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/*toduct= "Arabidopsis thaliana OBP3 protein"
/transl_except= (pos:4811. .4909, aa:Gly-Gly)
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The invention relates to a transgenic plant transformed by a Dof transcription factor, OBF (ocs binding factor) binding protein (OBP3). OBP3 is also known as SOB1. The transgenic plant cell and OBP3 nucleic acid and polypeptides are useful in producing transgenic plants with altered size and stature and with normal and healthy root growth. The present sequence is Arabidopsis thaliana OBP3 DNA.
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                                             Sequence 7580 BP; 2376 A; 1376 C; 1291 G; 2537 T; 0 U; 0
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1080 1620 1680 1800 TGTGTGTCGACATAGTGAGGTCCATTAAAAAGAAGGTCTGATTAAAATTTTACGTTTGGAC CACAAATCTTTCTTTTAGAAATCGCGGACTGGGACACCCTTCCTACAACATGTCCGTCTTT GGTATAACATCAAGAATCACGAAAGAATTAAAAACTACCTGTCGAATCATGATTTGATT AACATGCAAAAGAATATATAGATTTACCGTATCAGATTTTCATACAATTTTTATATTTTT TCCAATAGATGAAGACATTATCACTCAGGTTCAGCTACTTCGAAGCGCAACATATCGACA ACTAATCTTACGTACCCCTCACATTCGTAACCATAAAATCATCAAATATAATAGAGAC TGGTGATCATAATTCGAAATATTTTCACTAATTCAATGTTATCGGTAAGTTATTAGG TGAGCTTGAAAGATTAACATGACAAACTGTATCGTGTGTCTCCTCGTCTATTCACCCCTAGA TATACACACTCCCCACAAATATAACCACAATATATATTGGTTACTACGAAATTCCAAT TATITITCIGGTAAAAACAICTIGATTAIGAACTATATAGTTAGGGATAIGTTIGAIGT

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QY 5753 TAACCCACGAGAATTATGCACCTAAATTCAGACTAATCCCCCAAATTTCAGAAATTTATG 5812 DD 1321 TAACCCACGAGAATTATGCACCTAAATTCAGACTAATCCCCCAAATTTCAGAAATTTATG 1380 QY 5813 TATTTTGCGAATTAATATGTTCACCAATCATAATGCCCAACTAATGAAAAGA 5872 DD 1381 TATTTTGCGAATTAATATGTTCACCAATCATAATGCACTAATGAAACAAAAAAAA	RESULT 3 ABQ73047 c ID ABQ73047 standard; DNA; 10078 BP. XX XX XX ABQ73047; XX XX XX Tomato anthocyanin 1 (ANT1) related plasmid pAG3202 SEQ ID NO:3. XX XX XX Tomato; ANT1; anthocyanin 1; Lycopersicon esculentum; plant; colour; XX
181 GATTACAATTCAAGCAACACTGGATTAGATTTTTGGTGAACTCAAATAGCAACAGAA 4735	TGTTGGTTGGGGTGTAATTTGGTGCTTGTCGGGGTTATTGCTGGGGAAGATCAACC TGTTGGTTGGGGTGTAATTTTGGTGCTTGTCGGGGTTATTGCTGGGGAAGATCAACC TGTTGGTTGGGGTGTAATTTTGAGGCTCAAAGGAAAGG

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The invention comprises a plant gene activation vector that contains a hairy-root induction gene and enhancer and/or promoter which can function
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which is responsible for many red and blue colours in plants. The polynucleotide is useful for modifying e.g. leaf colour, flower colour fruit colour in plants. The present sequence represents the plasmid pAG3202 which is used in an example from the present invention for the generation of plants with an ANTI phenotype by transformation with an activation tagging construct
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18.5%; Score 1402.4; DB 6
Best Local Similarity 99.9%; Pred. No. 1.3e-207;
Matches 1403; Conservative 0; Mismatches 1;
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                                                                            6177 TIGITICGGAICTAGATATCACATCCACTIGCTTTGAAGACGTGGTTGGAACGTCT
                                                                                       TCTTTTTCCACGATGTTCCTCGTGGGGGTCCATCTTTGGGACCACTGTCGTAGAG
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                                                             Gaps
                           Sequence 17511 BP; 4453 A; 4201 C; 4511 G; 4344 T; 0 U; 2 Other;
  in a plant. The vector of the invention is useful for analyzing gene. The present DNA sequence is claimed in the invention.
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                                           Query Match 18.0%; Score 1367.4; DB 14; Lengt
Best Local Similarity 99.9%; Pred. No. 3.4e-202;
Matches 1368; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene activation vector-related DNA sequence pHR-AT-GFP - SEQ ID 14.
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                                                                                                                                                                                                                                                                                                      TTTTCCACGATGTTCCTCGTGGGTGGGGTCCATCTTTGGGACCACTGTCGGTAGAGGCA
                                                                                                               TCTACTGTCCTTTCGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGGTTTCCC
                                                                                                                                                                                                                                                                                                                                                                     GATATTACCCTTTGTTGAAAAGTCTCAATAGCCCTCTGGTCTTCTGAGACTGTATCTTTG
TTGGGGATCTAGATATCACATCAATCCACTTGCTTTGAAGACGTGGTTGGAACGTCTTCT
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Best Local Similarity 99.9%; Pred. No. 3.4e-202;
Matches 1368; Conservative 0; Mismatches 1; Indels 0; G
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The desired trait may be increased resistance to the desired trait. The method is modified leaf number, leaf pigmentation and shape, modified leaf number, leaf pigmentation and shape, modified leaf number, solver number, con the plants having short life cycles are transformed, as cort are and shape, modified seen nordes, root mass or root covered by any ariseties or increased drought, salt and antibiotic commulified by any ariseties or increased drought, salt and antibiotic commulified by any ariseties or increased drought, salt and antibiotic commulified by any ariseties or increased drought, salt and antibiotic commulified by any ariseties or increased transformed, as
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/note= "129 bp fragment of the CaMV sequence"
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//ore= "additional 7 bp not associated with 35S enhancer"
1018. .1354
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                                                                                                                                                                                                                                                        not associated with 35S
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100.0%; Pred. No. 4.2e-201;
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/note= "CaMV 35S enhancer unit
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/note= "129 bp fragment
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Matches 1360; Conservative
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1360 GTTTCGGATCTAGATATCACATCCACTTGCTTTGAAGACGTGGTTGGAACGTCTTC 6239 TITITICCACGATGTICCTCGTGGGGGGTCCATCTTTGGGACCACTGTCGGTAGAGGC

TCGGATCTAGATATCACATCCACTTGCTTTGAAGACGTGGTTGGAACGTCTTC

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                                                                                    TATTACCCTTTGTTGAAAAGTCTCAATAGCCCTCTGGTCTTCTGAGACTGTATCTTTGAT
                                                                                                   100 TATTACCCTTTGTTGAAAAGTCTCAATAGCCCTCTGGTCTTCTGAGACTGTTTGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New transgenic plant cell, useful in producing plants with altered size and stature and with normal and healthy root growth.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 TCAAAGTGTGAGTATGTTTATTGGTTGGCTTCTGGTGATATTTATGTTTATTAGAATTT
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14.0%; Score 1062; DB 12;
Best Local Similarity 100.0%; Pred. No. 5.1e-155;
Matches 1062; Conservative 0; Mismatches 0;
                                                                                                                                                                               Arabidopsis thaliana OBP3 antisense DNA #9.
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                                                            ADL71848 standard; DNA; 1062 BP
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New transgenic plant cell, useful in producing plants with altered size and stature and with normal and healthy root growth.
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                                                                                                                                                                                                                                                                                                   781 AATTITCTCTTIGGTTAGATTTTTACACCGCCATGGAATTATCACTTCAAAAAATAAAAAA
                                                                                                                                                         841 GTTTAAAGTTACTATGACTTTAATCTGAGTTATTTATCCATTTTTGTTTTGTGAGCTTTGT
3765 TAAAAACCTTTTTTCTTGTCTTCTCCCAAGGGCTTATGTATAATGTTTTTCTTACAGGATT
                  GTTTAAAGTTACTATGACTTTAATCTGAGTTATTTATCCATTTTCTTTTGCAGCTTTGT
                                                                                                                                                                                                          3945 IGAAAAACTATAATTAATCTGCAATTCTTGTCAAAGTAGTCACAATTTTTATCTATTTTC
                                                                                                                                                                                                                                          901 IGAAAAACTATAATTIAATCIGCAATTCTIGTCAAAGTAGTCACAATTTTTATCTATTTTC
                                                                                                                                                                                                                                                                             TITIGICICCGACCAAIGITICAAACICGAAICCTITCGTIAAAAGITGITITCIGCTITA
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100.0%; Pred. No. 4.1e-128;
ative 0; Mismatches 0;
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Matches 888; Conservative
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14.0%; Score 1058; DB 12;
Best Local Similarity 100.0%; Pred. No. 2.1e-154;
Matches 1058; Conservative 0; Mismatches 0;
                                                                                                                                                                        Claim 39; SEQ ID NO 19; 53pp; English
                (UNIW ) UNIV WASHINGTON
                                                                                   WPI; 2004-225757/21.
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Pineda O,

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New plant transcription factor polynucleotides and polypeptides, useful in producing transgenic plants with commercially valuable properties, such as an alteration in a plant growth characteristic, e.g. growth rate
                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 406; 454pp; English.
                                                                                                                                                                                         (MEND-) MENDEL BIOTECHNOLOGY INC
                                                                                                                   09-AUG-2001; 2001US-0310847P.
19-NOV-2001; 2001US-0336049P.
11-DEC-2001; 2001US-0338692P.
                                                                                                                                                              14-JUN-2002; 2002US-00171468
           Arabidopsis thaliana.
                                                                                                                                                                                                                                                                         2003-248221/24.
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P-PSDB; ADD30378.
                                     WO2003013227-A2
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Pilgrim ML, J
Broun PE;
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                                                                                                                                                                                                                                    241 GIGGTCTCGACTGATAATACTACTACTTCATCACTTACTTCTCGCCCAAGTTACTCA
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            ATGGTGGAACGTGCTCGGATCGCAAAAGTCCCATTGCCTGAAGGCTCTAAATTGCCCT
                                                   AGATGTGACTCAACCAATACTAAGTTCTGTTACTTCAATAACTATAGCCTTACTCAACCT
                                                                     AGATGTGACTCAACCAATACTAAGTTCTGTTACTTCAATAACTATAGCCTTACTCAACCT
                                                                                                          CGCCATTTCTGCAAAACATGTCGTCGCTATTGGACACGTGGCGGTTCCTTGAGGAATGTT
                                                                                                                                                               CCTGTTGGAGGAGGCTTTAGGAGGAACAAGAAAGCAAATCCAAGATCGAAATCTACGGTC
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The invention relates to a number of isolated Arabidopsis thaliana CDNA sequences and their encoded proteins which are especially transcription factor related CDNA's and proteins. The isolated or recombinant plant transcription factor polymuclectides and polypeptides are useful in producing transgenic plants with commercially valuable properties, i.e. modified or altered desirable traits as compared to a reference plant, such as an alteration in a plant growth characteristic, e.g. growth rate, germination rate of seeds, vigor of plants and seedlings, or leaf and flower sensecence. Sequence information related to the polymucleotides and polypeptides can also be used in bioinformatic search methods. The transgenic plant is useful for growing a progeny plant from a parent plant. This sequence represents one of the CDNAs of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 CGCCATTTCTGCAAAACATGTCGTCGTCGTTGGACACGTGGCGGTTCCTTGAGGAATGTT
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                                                                                                                                                                                                                                                                                                                                                                                                       Length 795;
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Pred. No. 8.2e-98;
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les 795; Conservative
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ds; transcription factor; transgenic plant; growth rate; senescence; seed germination rate; plant vigor; seedling vigor.

Plant yield-related polynucleotide clone G1906,

(first entry)

15-JAN-2004

ADD30377;

BP

795

CDNA;

ADD30377 standard;

ADD30377

RATCLIFFE O. ADAM L J.
REUBER T L.
KEDDIE J.
BROUN P E.
PILGRIM M L.

(RATC/)
(ADAM/)
(REUB/)
(KEDD/)
(BROU/)
(PILG/)
(DUBE/)
(PINE/)
(YUGG/)

DUBELL A N. PINEDA O. YU G.

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5071
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transgenic; plant; enhanced tolerance to abiotic stress; glyphosphate tolerance; hormone sensitivity; disease resistance; sugar sensing; flowering; flower structure; stem bifurcation; branching pattern; apical dominance; trichome; stem morphology; root growth; root hair; seed development; cell proliferation; cell differentiation; premature senescence; necrosis; plant size; leaf morphology; seed morphology; seed biochemistry; root anthocyanin; plant anthocyanin; light response; shade avoidance; bioinformatic; transcription factor; ds.
421 GGAACTCAAATAAGCAACATGATAAGTGGTATGAGTTCTAGTGGTGGGGATCTTGGATGCA
                                                                                                                                                                                                481 TGGAGAATACCTCCATCACAACAAGCTCAGCAATTCCCTTTCTTGATCAACACTACCGGA
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                                                                                       GGAACTCAAATAAGCAACATGATAAGTGGTATGAGTTCTAGTGGTGGTGGATCTTGGATGCA
                                                                                                                                                                          TGGAGAATACCTCCATCACAAGCTCAGCAATTCCCTTTCTTGATCAACACTACCGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                     4892 GATTTTTCTTCAGGCGGGGTTAGCGCCACGCAACAAGAAATGTGAAGGCGGAAGAAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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RIECHMANN J L.
JIANG C.
HEARD J E.
HAAKE V.
CREELMAN R A.
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The invention describes a transgenic plant comprising a recombinant polynucleotide of any one of more than 500 nucleotide sequences fully defined in the specification or its complement. The method of the defined in the specification or its complement. The method of the chanced to be used to produced a plant having altered traits such as: enhanced tolerance to abiotic stress; glyphosphate tolerance; hormone sensitivity; disease resistance; sugar sensing; early or late flowering; altered flower structure, change in stem bifurcations, altered branching pattern, reduced apical dominance, reduced trichome density; lack of trichomes; reduced ectopic trichome development; altered trichome trichomes; reduced ectopic trichome number; altered stem morphology; increased root growth; increased root hairs; altered seed development; altered cell proliferation or cell differentiation; rapid development; altered cell proliferation or cell differentiation; rapid development; contenses in root anthocyanins; increase in plant size; leaf morphology; seed biochemistry; increase in root anthocyanins; increase in plant size; decreased plant size; leaf morphology; seed conforming or alteration in light response or shade avoidance. The transgenic plant, polynucleotides and polypeptides are useful in bioinformatic search methods. This sequence represents a plant transgenic place are deful in bioinformatic search methods. This sequence represents a plant
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                                                                                                                                                                                                                                                                                                                              New transgenic plant comprising a recombinant polynucleotide of any one of more than 500 nucleotide sequences, useful in bioinformatic search methods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 AGATGTGACTCAACCAATACTAAGTTCTGTTACTTCAATAACTATAGCCTTACTCAACCT
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                                                                                                                                                                                                               Broun PE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4232 ATGGTGGAACGTGCTCGGAATCGCAAAAGTCCCATTGCCTGAAGCAGCTCTAAATTGCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 Argergaacgrecregarcgcaaaagrecearrgecreaagcagcretaaarrgecer
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89.5%; Pred. No. 8.2e-98;
tive 0; Mismatches 0; Indels 9:
                                                                                                                                                                                            Haake V;
Keddie J,
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                                                                                                                                                                                          Riechmann JL, Jiang C, Heard JE,
Ratcliffe O, Adam LJ, Reuber TL,
Dubell AN, Pineda O, Yu G;
                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 2767; 435pp; English.
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Matches 795; Conservative
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P-PSDB; ADI44305.
                                                                                                                                                                                              Sherman BK,
Creelman RA,
                                                                                                                                                                                                                                   Pilgrim ML,
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                                                                   Local Similarity
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                                      TGGAGAATACCTCCATCACAACAAGCTCAGCAATTCCCTTTCTTGATCAACACTACCGGA
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                                                                                                                                                                                                                                             Transgenic plant; Dof transcription factor; ocs binding facto; plant size; plant stature; root growth; plant; gene; ds; OBF; OBF binding protein; OBF3; SOB1; mouse-ear cress.
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                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana OBP3 antisense DNA #4.
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                                                                                                                                                                                                                                                                                                  ADL71843 standard; DNA; 684
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                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana
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transcription factor, OBF (ocs binding factor) binding protein (OBP3). OBP3 is also known as SOB1. The transgenic plant cell and OBP3 nucleic acid and pollypeptides are useful in producing transgenic plants with altered size and stature and with normal and healthy root growth. The present sequence is Arabidopsis thaliana OBP3 antisense DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AACGAGGAATACACATCATGGGGGGGTAACAGTTCTTGGACCGGTTTCACCTCCAACAAC
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                                                                                                                                                             Length 684;
                                                                                                                       Sequence 684 BP; 212 A; 145 C; 149 G; 178 T; 0 U; 0 Other;
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                                                                                                                                                           9.0%; Score 684; DB 12;
100.0%; Pred. No. 1.4e-96;
tive 0; Mismatches 0;
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Production method of a large amount of biologically active interleukin-12 protein using plant cell suspension culture cheaply and safely.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         interleukin-12; transgenic plant; Nicotiana tabacum; T-DNA; pMYL28; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     503 ATAGCCCTTTGGTCTTCTGAGACTGTATCTTTGATATTCTTGGAGTAGACGAGAGTGTCG
                                       7224 ACTIGCITIGAAGACGIGGTIGGAACGICTICITITICCACGAIGTICCICGIGGGIGG
                                                                                                                           7464 ATAGCCCTCTGGTCTTCTGAGACTGTATCTTTGATATTCTTGGAGTAGACGGGAGTGTCG
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                   623 CAATGATGGCATTTGTAGGTGCCACCTTCCTTTTCTACTGTCCTTTTGATGAAGTGACAG
                                                                                                                                                                                                                                                                                                                                                             7404 ATAGCTGGGCAATGGAATCCGAGGAGGTTTCCCGATATTACCCTTTGTTGAAAAGTCTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence shows the nucleotide sequence for the plasmid designated pPHI1406. The plasmid vector contains the gene for MCDV (maize chlorotic dwarf virus) coat protein 3 placed under control of trandem cauliflower modaic virus 35S promoters isolated from the 1841 strain of the virus, and a polyA signal sequence obtained from the potato proteinase inhibitor I ( Pin II) gene that exhibits enhancer-like activity. The chimeric gene also includes a 79 bp sequence omega' from the 5' leader region of tobacco mosaic virus that functions as a translational enhancer; and a zea mays alcohol dehydrogenase 1, intron 1 fragment spanning nucleotides 119-67, trimmed to 557 bp with Bal 31 nuclease, which has been shown to function as an enhancer of gene expression in monocots. The DNA is used for imparting resistance to MCDV or viruses to which MCDV infection or resistance provides cross-resistance, including maize dwarf mosaic virus strain A Any or all of the three coat protein genes from MCDV can be used to provide protection for plants. MCDV has a single, long RNA core which is shown in AAQ74694. (Updated on 25-MAR-2003 to correct PN field.)
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1043 TGCTCCTCGTGGGTGGGGGGTCCATCTTTGGGACCACTGTCGGCAGAGGCATCTTGAACGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1103 AGATATCACATCCACTTGCTTTGAAGACGTGGTTGGAACGTCTTCTTTTCCACGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA encoding maize chlorotic dwarf virus proteins - used to provide plants with resistance to the virus and related viral infections.
                                                                                                                           119. .672
/*teg= a
/note= "zea mays alcohol dehydrogenase 1, intron
fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 5033;
resistance; viral infection resistance; maize plant; dwarf mosaic virus; MDMV; ds.
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8.2%; Score 621; DB 2;
Best Local Similarity 95.1%; Pred. No. 8.5e-87;
Matches 653; Conservative 0; Mismatches 30
                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mcmullen MD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 2; Page 14-17; 40pp; English.
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p40; (c) isolating calluses of the transgenic plant of step (b) to produce a plant cell line(KCTC 1021BP); and (d) suspension culturing the plant cell line(KCTC 1021BP) to express the biologically active interleukin-12, wherein the plant is Nicotiana tabacum; gelatin may be further added into the medium in step (d) for improving production of IL-12; and the IL-12 contains a signal peptide. The present sequence represents T-DNA region of pWYLZ8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GATGGCATTIGTAGAAGCCATCTICCTTTTCTACTGTCCTTTCGATGAAGTGACAGATAG
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Best Local Similarity 93.6%; Pred. No. 3.3e-86;
Matches 659; Conservative 0; Mismatches 33
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Search completed: December 30, 2005, 17:26:48 Job time: 2706 secs

November 2005

Published Applications Nucleic Acid and Published Applications Amino Acid database searches now generate two sets of results each. The Published Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published Applications produce two sets of results, with the extensions ripbm (Published Applications NA Main) and ripbm (Published Applications NA New). Searches run against Amino Acid Published Applications produce two sets of results, with the extensions rapbm (Published Applications AA Main) and rapbm (Published Applications AA New).

VACO TIAN IIAVA TODO

	GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.
OM nucleic - nuc	- nucleic search, using sw model
Run on:	December 30, 2005, 17:26:56; Search time 470 Seconds (without alignments) 8454.579 Million cell updates/sec
Title: Perfect score: Sequence:	US-10-650-249-1 7580 1 agctctattaattcaagagagccgccaccgcggtggagct 7580
Scoring table:	IDENTITY NUC Gapop 10 ⁻ 0 , Gapext 1.0
Searched:	4172979 segs, 262114271 residues
Total number of	hits satisfying chosen parameters: 8345958
Minimum DB seg Maximum DB seg	seq length: 0 seq length: 200000000
Post-processing	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	.	122, App	Appli	Appl	Appl	App1	Appl	App1	Appli	Appl	Appl	, Appl	ppli	App1	App1	App1	Appl	Appl	Appl	Appl	Appl	Appl	ppli	Appl
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	Description	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
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SUMMARIES		US-10-508-263-122	US-11-038-981A-1	JS-11-038-981A-23	JS-11-192-801-23	US-11-192-801-15	11-038-981A-21	11-038-981A-22	JS-11-038-981A-6	11-192-801-13	JS-10-391-414-10	JS-11-038-981A-26	11-038-981A-5	JS-11-038-981A-18	11-038-981A-20	11-038-981A-19	11-038-981A-25	11-038-981A-24	JS-11-038-981A-27	11-038-981A-28	JS-11-038-981A-29	JS-10-927-641-40	JS-10-509-691-1	JS-11-121-086-25
SUMMA		10-50	11-03	11-03	11-19	11-19	11-03	11-03	11-03	11-19	10-39	11-03	11-03	11-03	11-03	11-03	11-03	11-03	11-03	11-03	11-03	10-92	10-50	11-12
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	Score	617.2	381.2	379.2	377.6	377.6	376.2	374.6	373.6	367.2	303.6	118	116.2	116.2	116.2	116.2	116.2	116.2	116.2	116.2	116.2	101.6	88.6	78.2
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         6490 AGTAGACGAGAGTGTCGTGCTCCACCATGTTGGGGGATCTAGATATCACATCCACTT
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                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Conner, Timothy W.
APPLICANT: Conner, Timothy W.
APPLICANT: Pang, Sheng Z
APPLICANT: Pang, Sheng Z
APPLICANT: You, Jinsong
: TITLE OF INVENTION: CHIMERIC PROMOTERS FOR USE IN: FILE REPRENCE: 38-21(51446)B
: CURRENT APPLICATION NUMBER: US/11/038,981A
: CURRENT FILING DATE: 2005-01-20
: PRIOR APPLICATION NUMBER: 60/537,793
: SEQ ID NO 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Artificial promoter sequence US-11-038-981A-23
                                                                                                                                                                                                                                                                                                                                                                  Sequence 23, Application US/11038981A, publication No. US20050283856A1, GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                       RESULT 3
US-11-038-981A-23/c
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                                              GCTTTGAAGACGTGGAACGTCTTCTTTTCCACGATGTTCCTCGTGGGGGGGTC
                                                                         764 GCTTTGAAGACGTGGAACGTCTTTTTTCCACGATGCTCCTCGTGGTGGGGTC
                                                                                                         CATCTTTGGGACCACTGTCGGTAGAGCCATCTTGAACGATAGCCTTTCCTTTATCGCAAT
                                                                                                                           GATGGCATTTGTAGGTGCCACCTTCCTTTTCTACTGTCCTTTTGATGAAGTGACAGATAG
                                                                                                                                                                                                                                CTGGGCAATGGAATCCGAGGAGGTTTCCCGATATTACCCTTTGTTGAAAAGTCTCAATAG
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                                                                                                                                                                                                                                                                                                                                                          CCACCATGTTGGGGATCCACTAGTTCTAGAGCGGCCGCCACCGC 7571
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US-11-038-981A-1/C
is Sequence 1, Application US/11038981A
is Sequence 1, Application Wo. US20050283856A1
is GENERAL INFORMATION:
is APPLICANT: Conner, Timothy W.
is APPLICANT: Pang, Sheng Z
is APPLICANT: Pang, Sheng Z
is TITLE OF INVENTION: CHIMERIC PROMOTERS FOR USE IN PLAN
FILE REPRENCE: 38-21(51446)B
is CURRENT FILING DATE: 2005-01-20
is PRIOR FILING DATE: 2005-01-20
is ROW APPLICATION NUMBER: 60/537,793
is ROW RILING DATE: 2004-01-20
is NUMBER OF SEQ ID NOS: 35
is ENGTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 381.2; DB 7;
Pred. No. 1.2e-56;
0; Mismatches 33;
                 AGTAGACGAGAGTGTCGTGCTCCACCATGT
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Matches 489; Conserv
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US-11-038-981A-1
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Sequence 15, Application US/11192801
| Publication No. US20050273882A1
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: Romano. Charles P. |
| TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants |
| FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn |
| CURRENT APPLICATION NUMBER: US/11/192,801 |
| CURRENT PILING DATE: 2005-07-29 |
| PRIOR APPLICATION NUMBER: US/10/232,665 |
| PRIOR FILING DATE: 1999-08-19 |
| PRIOR FILING DATE: 1999-08-19 |
| NUMBER OF SEQ ID NOS: 43 |
| SOFTWARE: Patentin Ver. 2.0
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AGATATCACATCAATCCACTTGCTTTGAAGACGTGGTTGGAACGTCTTCTTTTTCCACGA 494
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                                                               493 TGCTCCTCGTGGGTGGGGGTCCATCTTTGGGACCACTGTCGGCAGAGGCATCTTCAACGA
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LOCATION: (25)...(640)
OTHER INFORMATION: P-CAMV.35S
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OTHER INFORMATION: I-Zm.Hsp70
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LOCATION: (1490)..(3448)
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US-11-192-801-15/c
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Publication No. US20050273882A1

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants

FILE REFRENCE: 38-21 (15304) Cry3Bb Improved Exp. Corn

CURRENT APPLICATION NUMBER: US/11/192,801

CURRENT FILING DATE: 2005-07-29

PRIOR APPLICATION NUMBER: US/10/232,665

PRIOR APPLICATION NUMBER: US/10/232,665

PRIOR APPLICATION NUMBER: US/09/377,466

PRIOR FILING DATE: 1999-08-19

NUMBER OF SEQ ID NOS: 43

SEQ ID NOS: 43

SEQ ID NO 23
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                                                                                                                          CTCGTGGGTGGGGTCCATCTTTGGGACCACTGTCGGCAGAGGCATCTTCAACGATGGCC
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                                                                                                   CTCGTGGGTGGGGGTCCATCTTTGGGACCACTGTCGGTAGAGGCATCTTGAACGATAGCC
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OTHER INFORMATION: Cry3Bb1 variant 11231mv2
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NAME/KEY: terminator
LOCATION: (3217)..(3450)
COTHER INFORMATION: T-Ta.hspl7
US-11-192-801-23
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NAME/KRY: promoter
LOCATION: (25)...(640)
OTHER INFORMATION: P-CaMV.35S
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NAME/KEY: S'UTR
LOCATION: (664)..(734)
OTHER INFORMATION: L-Ta.hcbl
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OTHER INFORMATION: I-OS.Act1
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Best Local Similarity
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NAME/KEY: intron
LOCATION: (748)...
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US-11-192-801-23/c
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NAME/KEY: CDS
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308 TACCCTTTGTTGAAAGTCTCA----
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                                                       Query Match
Best Local Similarity
Matches 486; Conserv
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US-11-038-981A-22/c
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                                                                                                                                                                                                                                                                                           TAGCCTTTCCTTTATCGCAATGATGGCATTTGTAGAAGCCATCTTCCTTTTCTACTGTCC 6369
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                                                                                                                                               Gaps
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                         NAME/KEY: terminator
LOCATION: (3475)..(3730)
OTHER INFORMATION: Agrobacterium tumefaciens nos 3' transcription
OTHER INFORMATION: termination and polyadenylation sequence
                                                                                                                                            77;
                                                                                                              Score 377.6; DB 7; Length 3754;
Pred. No. 8.9e-56;
0; Mismatches 34; Indels 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 21, Application US/11038981A

Publication No. US20050283856A1

GENERAL INFORMATION:
APPLICANT: Conner, Timothy W.
APPLICANT: Flashiski, Stanislaw
APPLICANT: Pang, Sheng Z
APPLICANT: Pang, Sheng Z

TITLE OF INVENTION: CHIMERIC PROMOTERS FOR USE IN PLANTS
FILE REFERENCE: 38-21(51446)B

CURRENT APPLICATION UNMBER: US/11/038,981A

CURRENT PILING DATE: 2005-01-20

PRIOR FILING DATE: 2004-01-20

NUMBER OF SEQ ID NOS: 35

SEQ ID NO 21

LENTH: 1467
INFORMATION: Cry3Bbl variant v11231
                                                                                                                 5.0%;
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                                                                                                                                             Matches 485; Conservative
                                                                                                                                Similarity
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US-11-038-981A-21/c
                                                                        ; OTHER INFORM
US-11-192-801-15
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                                                                                                                         Gaps
                                                                                                                       77;
                                                                          Length 1467
                                                                                                                       Indels
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Publication No. US20050283856A1
GENERAL INFORMATION:
APPLICANT: Conner, Timothy W.
APPLICANT: Flasinski, Stanislaw
APPLICANT: Paginski, Stanislaw
APPLICANT: Paginski, Stanislaw
APPLICANT: Paginski, Stanislaw
APPLICANT: Pou, Jinsong
TITLE OF INVENTION: CHIMERIC PROMOTERS FOR USE IN PLA
FILE REFERENCE: 38-21(51446)B
CURRENT APPLICATION NUMBER: US/11/038,981A
CURRENT PILING DATE: 2005-01-20
PRIOR PILING DATE: 2004-01-20
NUMBER OF SEQ ID NOS: 35
                                                                                                                       38;
                                                                       DB 7;
                                                                     5.0%; Score 376.2; DB 7
llarity 80.9%; Pred. No. 1.2e-55;
Conservative 0; Mismatches 38
; OTHER INFORMATION: Artificial promoter sequence US-11-038-981A-21
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Gaps

77;

Indels

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34;
Mismatches
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LOCATION: (25)..(640)
OTHER INFORMATION: P-CaMV.35S
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                                                                                                                                                                                                                                                                                    284 TTGAAAGTCTCA----
  Conservative
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US-11-192-801-13/c
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LENGTH: 4149
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                                                                                     Gaps
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                                                                                     77;
                                                           Length 1467;
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Publication No. US20050283856A1
GENERAL INFORMATION:
APPLICANT: Conner, Timothy W.
APPLICANT: Flasinski, Stanislaw
APPLICANT: Plasinski, Stanislaw
APPLICANT: Pang, Sheng Z
APPLICANT: Pang, Sheng Z
APPLICANT: Pang, Sheng Z
TITLE OF INVENTION: CHIMERIC PROMOTERS FOR USE IN PLANTS
FILE REFERENCE: 38-21(51446)B
CURRENT APPLICATION NUMBER: US/11/038,981A
CURRENT FILING DATE: 2005-01-20
PRIOR FILING DATE: 2004-01-20
PRIOR FILING DATE: 2004-01-20
NUMBER OF SEQ ID NOS: 35
SEQ ID NO 6
LENGTH: 524
                                                         Score 374.6; DB 7; Length: Pred. No. 2.2e-55; 0; Mismatches 34; Indels
                                                                                                                 6193 TATCACATCAATCCACTTGCTTTGAAGACGTGGAACGTCTTCT

    FEATURE:
    OTHER INFORMATION: Artificial promoter sequence
US-11-038-981A-22

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                                                         Query Match
Best Local Similarity 81.3%;
Matches 482; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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Sequence 13, Application US/11192801

Publication No. US20050273882A1

GENERAL INFORMATION:
APPLICANT: Romano. Charles P.
TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
CURRENT APPLICATION NUMBER: US/11/192,801

CURRENT FILING DATE: 2005-07-29

PRIOR FILING DATE: 2002-08-29

PRIOR FILING DATE: 1999-08-19

NUMBER OF SEQ ID NOS: 43

SOFTWARE: Patentin Ver. 2.0
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CCTCGTGGGTGGGGTCCATCTTTGGGACCACTGTCGGTAGAGGCATCTTGAACGATAGC
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                                                                                                                                                                                                                                                                                   LOCATION: (3871)..(4127)
OTHER INFORMATION: T-AGRtu.nos 3' transcription termination and OTHER INFORMATION: polyadenylation sequence
                                                                                                                                                                                                                                                                                                                                                         Length 4149;
                                                                                                                                                                                                                                                                                                                                                                                         33; Indels
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81.4%; Pred. No. 5.5e-54;
tive 0; Mismatches 33;
                                                                                                                                                NAME/KEY: transit peptide
LOCATION: (1799)..(1885)
OTHER INFORMATION: carboxy terminus TS-Zm.rbcS
                                           LOCATION: (1489). (1535)
OTHER INFORMATION: amino terminal TS-Zm.rbcS
                                                                                                                                                                                                          NAME/KEY: CDS
LOCATION: (1885)..(3843)
OTHER INFORMATION: Cry3Bb1 variant v11231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               313 TTTGTTGAAAGTCTCA------
OTHER INFORMATION: I-Zm. Hsp70
                                                                                     NAME/KEY: intron
LOCATION: (1636)..(1798)
OTHER INFORMATION: I-Zm.rbcS
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 81.49
Matches 485, Conservative
            FEATURE:
NAME/KEY: trangit peptide
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NAME/KEY: terminator
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US-11-192-801-13
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Sequence 10, Application US/10391414 Publication No. US20050278799A1

RESULT 10 US-10-391-414-10/c

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APPLICANT: KATSURA, Koji
APPLICANT: IV. Yusuke
TITLE OF INVENTION: Stress Induced Promoter Derived From Rice
TITLE OF INVENTION: Stress Induced Promoter Derived From Rice
CURRENT APPLICATION NUMBER: US/10/391,414
CURRENT APPLICATION NUMBER: US/202-3377316
PRIOR PILING DATE: 2002-12-26
PRIOR FILING DATE: 2002-12-26
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PATCHIN Ver. 2.1
IEBNGTH: 835
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APPLICANT: Flasinski, Stanislaw
APPLICANT: Pang, Sheng Z
APPLICANT: Pang, Sheng Z
TITLE OF INVENTION: CHIMERIC PROMOTERS FOR USE IN PLANTS
TITLE OF INVENTION: CHIMERIC PROMOTERS FOR USE IN PLANTS
FILE REFERENCE: 38-21(51446)B
CURRENT FILING DATE: 2005-01-20
PRIOR APPLICATION NUMBER: 60/537,793
PRIOR FILING DATE: 2004-01-20
NUMBER OF SEQ ID NOS: 35
SEQ ID NO 26
LENGTH: 1935
                                                                                                                                                                                                                                                                                                                                                                                                                                      29; Indels
                                                                                                                                                                                                                                                                                                                                                                                     Query Match
4.0%; Score 303.6; DB 6;
Best Local Similarity 91.7%; Pred. No. 2.5e-43;
Matches 321; Conservative 0; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.6%; Score 118; DB 7; 78.0%; Pred. No. 1.8e-11;
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; OTHER INFORMATION: Artificial promoter sequence

US-11-038-981A-26
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                                                                                                                                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Cauliflower mosaic virus
US-10-391-414-10
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Best Local Similarity
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NUMBER OF SEQ ID NOS: 35
SEQ ID NO 18
LENGTH: 1273
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                                         6468 ACTGTATCTTTGATATTCTTGGAGTAGTAGACGAGAGTGTCGTGCTCCACCATGTTGGGGATC 6527
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                                                                             497 ACAGTAATATTTGTAAGCTTCGAAGGATAGTGGGATTGTGCGTCATCCCTTACGTCAGTG
                                                                                                                   6528 TAGATATCACATCAATCCACTTGCTTTGAAGACGTGGAACGTCTTCTTTTTCCACG
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Publication No. US20050283856A1

GENERAL INFORMATION:
APPLICANT: Conner, Timothy W.
APPLICANT: Flaatinski, Stanislaw
APPLICANT: Pang, Sheng Z
APPLICANT: Pang, Sheng Z
TITLE OF INVENTION: CHIMBRIC PROMOTERS FOR USE IN PLANTS
FILE REFERENCE: 38-21(51446)B
CURRENT APPLICATION NUMBER: 08/11/038,981A
CURRENT APPLICATION NUMBER: 60/537,793
PRIOR APPLICATION NUMBER: 60/537,793
PRIOR PILLING DATE: 2004-01-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 18, Application US/11038981A

Publication No. US20050283856A1

GENERAL INPORMATION:
APPLICANT: Conner, Timothy W.
APPLICANT: Planishki, Stanislaw
APPLICANT: Pang, Sheng Z
APPLICANT: Paug, Sheng Z

TITLE OF INVENTION: CHIMERIC PROMOTERS FOR USE IN PLANTS
FILE REFERENCE: 38-21(51446)B

CURRENT APPLICATION NUMBER: US/11/038,981A

CURRENT FILING DATE: 2005-01-20

PRIOR APPLICATION NUMBER: 60/537,793

PRIOR FILING DATE: 2004-01-20
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   40;
   Mismatches
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; ORGANISM: Cauliflower mosaic virus
US-11-038-981A-5
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0
   Matches 142; Conservative
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SEQ ID NO 5
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US-11-038-981A-18/c
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                                                                                                                                         Length 1273;
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APPLICANT: Flashiski, Stanislaw
APPLICANT: Flashiski, Stanislaw
APPLICANT: Pang, Sheng Z
APPLICANT: Pang, Sheng Z
APPLICANT: Pang, Sheng Z
CARENT: Pou, Jingurent PROMOTERS FOR USE IN PLANTS
FILE REFERENCE: 38-21(51446)B
CURRENT APPLICATION NUMBER: US/11/038,981A
CURRENT FILING DATE: 2005-01-20
PRIOR APPLICATION NUMBER: 60/537,793
PRIOR FILING DATE: 2004-01-20
NUMBER OF SEQ ID NOS: 35
SEQ ID NO 20
LENGTH: 1273
                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                         6190 AGATATCACATCCACTTGCTTTGAAGACGTGGTTGGAACGI
                                                                                                                                         Query Match 1.5%; Score 116.2; DB 7; Best Local Similarity 97.5%; Pred. No. 3.1e-11; Matches 118; Conservative 0; Mismatches 3;
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Pred. No. 3.1e-11;
                                                                  ; OTHER INFORMATION: Artificial promoter sequence US-11-038-981A-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Artificial promoter sequence
US-11-038-981A-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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; Sequence 19, Application US/11038981A
; Sequence 10. US-00500283856A1
; GENERAL INFORMATION:
; APPLICANT: Conner, Timothy W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 20, Application US/11038981A; Publication No. US20050283856A1; GENERAL INFORMATION:
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TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity
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papelicant: Flasinski, Stanislaw
papelicant: Pang Sheng Z
APPLICANT: Pang, Sheng Z
APPLICANT: Pang, Sheng Z
APPLICANT: You, Jinsong
FILE REPRENCE: 320 1 (11/038,981A
CURRENT PILIG DATE: 2005-01-20
FRIOR APPLICATION NUMBER: US/11/038,981A
CURRENT FILING DATE: 2005-01-20
FRIOR APPLICATION NUMBER: US/11/038,981A
CURRENT FILING DATE: 2005-01-20
FRIOR APPLICATION NUMBER: US/11/038,981A
CURRENT FILING DATE: 2005-01-20
FRIOR APPLICATION NUMBER: US/11/038
CURRENT FILING DATE: 2005-01-20
FRIOR APPLICATION NUMBER: US/11/038
COGANISM: Artificial Sequence
FRIUME NUMBER OF SEQ ID NOS: 35
CURRENT REPRENCE: 35
CURRENT APPLICATION NUMBER: US/11/038,981A
COGANISM: Artificial Sequence
FRIUME NUMBER OF SEQ ID NOS: 35
CURRENT REPRENCE: 300-01-20
FRIUME NUMBER: US/11/038,981A
FRIUME: US/11-038-981A-19
CURRENT REPRENCE: 300-01-20
FRIUME: US/11-038-981A-19
CURRENT REPRENCE: 35
CURRENT REPRENCE: 35
CURRENT APPLICATION NUMBER: US/11/038,981A
FRIUME: US/11-038-981A-19
CURRENT REPRENCE: 35
CURRENT REPRENCE: 35
CURRENT APPLICATION NUMBER: US/11/038,981A
FRIUME: US/11-038-981A-19
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CURRENT APPLICATION NUMBER: US/11/038,981A
FRIUME: US/11-038-981A-19
CURRENT REPRENCE: US/11/038,981A
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Search completed: December 31, 2005, 06:31:43 Job time : 477 secs

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LENGTH: 7580
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                                                                                                                                          December 30, 2005, 16:41:57; Search time 3569 Seconds (without alignments) 17562.871 Million cell updates/sec
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Sequence 92, Appl
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2: /cgn2_6/ptodataAl/pubpna/USO8_PUBCOMB.seq:*

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Sequence 89, Appl Sequence 2, Appli Sequence 5, Appli Sequence 95, Appli Sequence 95, Appli Sequence 109, Appl Sequence 109, Appl Sequence 109, Appl Sequence 10, Appli Sequence 10, Appli Sequence 10, Appli Sequence 11, Appli Sequence 12, Appli Sequence 12, Appli Sequence 13, Appli Sequence 14, Appli Sequence 17, Appli Sequence 18, Appli Sequence 19, Appli Sequence 11, Appli Sequence 11, Appli	Sequence 95, Appl Sequence 6, Appli Sequence 95, Appl Sequence 109, App Sequence 21, Appl
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ALIGNMENTS

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Sequence 1, Application US/10650249
Sequence 1, Application US/10650249
Publication No. US20040045055A1
GENERAL INFORMATION:
APPLICAMT: Neff, Michael M
TITLE OF INVENTION: THE GENE FOR A DOF TRANSCRIPTION FACTOR CAPABLE OF ALTERING
TITLE OF INVENTION: THE SIZE AND STATURE OF A PLANT
FILE REFERENCE: WSHU 2064.1
CURRENT APPLICATION NUMBER: US 60/406,657
PRIOR APPLICATION NUMBER: US 60/406,657
PRIOR APPLICATION NUMBER: US 60/406,657
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Version 3.1
SEQ ID NO
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; ORGANISM: Arabidopsis thaliana
US-10-650-249-1
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Best Local Similarity 100.
Matches 7580; Conservative
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	& 8	3781 IGTCTTCTCCAAGGGCTTATGTATAATGTTTTTCTTACAGGATTAATTTTCTCTTTGGTT 3840
	<i>₹</i> 8	3841 AGATTTTTACACCGCCATGGAATTATCACTTCAAAAATAAAAAGTTTAAAGTTACTATG 3900
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CGTATATGAGTTGGCAAAAATAAGCAAACAAAATACCTGTTCAAATACCACTTAAT TCCAAAAAGGTTAGTAATAAGTAAGAAGGCTTTTATTTAT	<i>&</i> 8	4201 TGCAGGTTCGAGTCAAGGTGAATTCAATGGTGGAACGTGCTCGGATCGCAAAGT 4260
TCCABABAGGITAGTARTAAGTAAGAAGSCITITAIITAGAAAACAAAAAGAAATGAAAA 318 AGCCTBAGAGAATGATGAAAATTGABAGAAAAAAGAGCATTGTTATAGAAAAAAAA 324	& 8	4261 CCCATTGCCTGAAGCAGCTCTAAATTGCCCTAGATGTGACTCAACCAATACTAAGTTCTG 4320
AGCCTARGAGAATGATGATAATTTGAAAGAGAAAAAGAGCATTGTTATAGAAAAAAAA	& 8	4321 TTACTTCAATAACTATAGCCTTACTCAACCTCGCCATTTCTGCAAAACATGTCGTCGCTA 4380
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TCTCTTTATCCCATTCAGCTCCTCCTTCTCTCTCTCTCTC	& g	4441 GAGAAGCAAATCCAGATCGAAATCTACGGTCGTGGTCTCGACTGATAATACTAGTAC 4500
CAATTCTTCTTCTTCTTCTAFGATATCCACCATATCTGCGACCTCTTACCTAAAAGGA 342 TACAAGTAAGAGATTCAAAGGTTTTCTCATCTCTTCCAGGAATCAGTTCGATTCC 348	₩	4501 TTGATCACTTACTTCGCCCAAGTTACTCAAACCCTAGCAAGTTTCATAGCTACGGTCA 4560
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3541 TTTTCCCCCAAGCTCGATCAAGATTTATGAAAATTTGATGAGATTTTGTTCGACAAAAT 3600	& —	4681 TATGAGTTCTAGTGGTGGGATCTTGGATGCATGGAGAATACCTCCATCACAACAAGGTCA 4740

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Matches 1743; Conservative 0; Mismatches 0; Indels 3; Gaps 4436 AACAAGGAAATCCAGATCGAAATCTACGGTCGTCGTCTCGACTGATAATACTACT	121 GGTCAAATCCCGGGGTTTAATTCCAACTTGCCCATCTTGCCTCTCCAAAGCCTTGG 180 4616 GATTACAATTCAAGCAACACTGGATTAGATTTTGGTGAACTCAAATAAGCAACACATGATA 4675	241 AGTGGTATGAGTTGTAGTGGGATCTTGGATGCATGGAGAATACCTCCATCACAACAA 4736 GGTCAGCAATTCCTTGATCAACACTACCGGATTGGTGCAACATCTTCAAACGCGTTA	DD 361 TATCCATTACTAGAAGGGAAGGGTTAATCCAGGGTTATCTCAGGAGGAGGTAGT 420 QY 4856 GATTATTCCAATCAGCTAATGTTTAAGCCCTTGATGGATTTTTCTTCAGGCGGGGTTAGC 4915 DD 421 GATTATTCCAATCAGCTAATGTTTAAGCCCTTGATGGATTTTTCTTCAGGCGGGGTTAGC 480 QY 4916 GCCACGCAACAACAAAGGTAAGGTTTAAGGATTCGGGGGGGTTAGC 4975 DD 481 GCCACGCAACAACAAAATGTGAAGGGGAAAGAATGATCAGGATCGGGTAGGATTCGG	4976 GATGGAGTGAATACTTATTCAAGAACTTTTTGGGTAATATCAACATAAGGGAGG	5096 TCAACAGGCCATCTCTCATTCTAAGTACTCAGGCACTAGCTATTCTTGATGATTCTTTT	Db 721 TGTTGGTTGGGTGTACATTGGTGCTTGTCATGCGAGTTATTGCTGAGGAAGATCAAACC 780 Oy 5213 ATGCAGCTATATCCAAAGGCTAATTTTGAGGCTCAAAGGAAAGGTATAAAAACTA 5272 Db 781 ATGCAGCTATATCCAAAGGCTAATTTTGAGGCTCAAAGGAAAGGTATGGTTATAAAAACTA 840 Oy 5273 TCTTTTGATCTTTTAAAAGATCTTCAAAGTGTGAGTATTTATT	Oy 5333 GAIATTTATGTTTTATTAGAATTTGGTCTTATATATATATATA
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TCGTCCAACTTATATACTCTGATTCTTATTTTTTTTTTT

	6539 TCATCCACTTGCTTGAAGACGTCGTTGGAACGTCTTTTTTCCACGATGTTCTCTCTC	GGGTGGGGGCCCATCTTGGGACCACTGTCGGTAGGGCATCTTGAACGATAGCCTTTCC TTTATCGCAATGATGGCATTTGTAGAAGCCATCTTCCTTTTCTACTGTCCTTTCGATGAA TTTATCGCAATGATGGCATTTGTAGAAGCCATCTTCCTTTTCTACTGTCCTTTCGATGAA	880 TITAICGCAAIGAIGGCAITIGIAGAAGCCAICTICCTITITCTACTGTCCTTTCGATGAA 821 6719 GIGACAGAAAGGCGGCAAIGGAATCCGAGGAGGTTTCCCGATATAACCCTTTGTTGAAA 6778	6779 AGTOTCAATAGCCCTCTGGTCTTCTGAGACTGTATCTTTGATATTCTTGGAGTAGACGAG 6838 	6839 AGTGTCGTCCACCATGTTGGGGATCTAGATATCACATCAATCCACTTGCTTTGAAGA 6898 	6899 CGTGGTTGGAACGTCTTTTTCCACGATGTTCCTCGTGGGTGG	6959 ACCACTGTCGGTAGAGGATCTTGAACGATAGCCTTTCCTTTATCGCAATGATGGCATTT 7018	7019 GTAGAAGCCATCTTCCTTTCTACTGTCCTTTCGATGAAGTGACAGATAGCTCGGCAATG 7078 	7079 GAATCCGAGGAGGTTTCCCGATATTACCCTTTGTTGAAAGTCTCAATAGCCCTCTGGTC 7138 460 GAATCCGAGGAGGTTTCCCGATATTACCTTTGTTGAAAAGTCTCAATAGCCCTCTGGTC 401		GGGGATCTAGATATCACATCAATCCACTTGCTTTGAAGACGTGGTTGGAACGTCTTCTTT 		TIGAAGGATAGCCTTTCCTTTATGGCAATGATGGATTTGTAGAAGCCATCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT		7439 TATTACCCTTGTTGAAAATCTCAATAGCCCTCTGGTCTTCTGAGACTGTATCTTTGAT 7498 100 TATTACCCTTTGTTGAAAAGTCTCAATAGCCTCTGGTCTTCTGAGACTGTATCTTTGAT 41 7499 ATTCTTGAGAGTAGAGAGTGTCGTCCACCACGTGTTG 7538	
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RESULT 6
US-10-650-249-20

Squence 20, Application US/10650249

Squence 20, Application No. US20040045055A1

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: THE SIZE AND STATURE OF A PLANT

FILE REPERENCE: WSHU 2604.1

CURRENT APPLICATION NUMBER: US/10/650,249

PRIOR APPLICATION NUMBER: US 60/406,657

PRIOR FILING DATE: 2002-08-02

NUMBER OF SEQ ID NOS: 20

SOFTWARE: Patentin version 3.1
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                                                                    Sequence 17, Application US/10650249
Publication No. US20040045055A1
GENERAL INFORMATION:
APPLICANT: Neff, Michael M
TITLE OF INVENTION: THE GENE FOR A DOF TRANSCRIPTION FACTOR CAPABLE OF ALTERING
TITLE OF INVENTION: THE SIZE AND STATURE OF A PLANT
FILE REFERENCE: WSHU 2064.1
CURRENT APPLICATION NUMBER: US/10/650,249
CURRENT FILING DATE: 2003-08-28
PRIOR FILING DATE: 2003-08-02
NUMBER OF SEQ ID NOS: 20
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.1
LENGTH: 1235
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US-10-650-249-17
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Query Match
14.0%; Score 1058; DB 7; L
Best Local Similarity 100.0%; Pred. No. 1.2e-182;
Matches 1058; Conservative 0; Mismatches 0;
FILE REFERENCE: WSHU 2064.1
CURRENT APPLICATION NUMBER: US/10/650,249
CURRENT FILING DATE: 2003-08-28
FRIOR APPLICATION NUMBER: US 60/406,657
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.1
SOFTWARE: PatentIn version 3.1
LENGTH: 1058
                                                                                 ; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-650-249-19
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Publication No. US20040045055A1
GENERAL INFORMATION:
APPLICANT: Neff, Michael M
TITLE OF INVENTION: THE GENE FOR A DOF TRANSCRIPTION FACTOR CAPABLE OF ALTERING
TITLE OF INVENTION: THE SIZE AND STATURE OF A PLANT
                                                                                                            5476
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                                       TCAAAGTGTGAGTATGTTTATTGGTTGGCTTCTGGTGATATTTATGTTTTATAGAATTT
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GENERAL INFORMATION:
APPLICANT: Mendel Biotechnology, Inc.
APPLICANT: MANCALEFE, Oliver
APPLICANT: RATCLIFFE, Oliver
APPLICANT: RATCLIFFE, Oliver
APPLICANT: RATCLIFFE, Oliver
APPLICANT: DUBELL, Arnold T
APPLICANT: BUREAD, Jacqueline E
APPLICANT: PILGRIM, Marsha L
APPLICANT: PILGRIM, Marsha L
APPLICANT: PILGRIM, Marsha L
APPLICANT: PILGRIM, Robert A
APPLICANT: PILGRIM, Robert A
APPLICANT: REGIONAN, Robert A
APPLICANT: PILGRIM, Robert A
APPLICANT: PILGRIM, Robert A
APPLICANT: PILGRIM, Pierre E
APPLICANT: PINEDA, Omaira
APPLICANT: PILGRIM, Pierre B
APPLICANT: PILGRIM, ROBER: US/10/225,066A
APPLICANT: PILGRIM BROWN, Pierre B
TITLE OF INVENTION VUMBER: US/10/225,066A
CURRENT APPLICATION NUMBER: 00/330,449
PRIOR PILING DATE: 2001-04-18
PRIOR FILING DATE: 2001-12-05
PRIOR PILING DATE: 2001-12-05
PRIOR PILING DATE: 2001-12-05
PRIOR PILING DATE: 2001-12-11
PRIOR PILING DATE: 2001-12-11
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 1122
SPETANEE PALENTIN VUMBER: 06/318,692
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 1122
SPETANEE PALENTIN VUMBER: 06/318,692
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4712 TGGAGAATACCTCCATCACAAGCTCAGCAATTCCCTTTCTTGATCAACACTACCGGA
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9.1%; Score 692; DB 6; Length 795;
Best Local Similarity 89.5%; Pred. No. 5.7e-116;
Matches 795; Conservative 0; Mismatches 0; Indels
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Sequence 12, Application No. US20040045055A1
Sequence 11, Application No. US20040045055A1
Sembla information.
Theory inversion in the Gene for a Dof Transcription factor capable of Altering TILLE OF INVERTION: THE GENE FOR A DOF TRANSCRIPTION FACTOR CAPABLE OF ALTERING TITLE OF INVERTION: THE SIZE AND STATURE OF A PLANT
FILLE REFERENCE: WSHU 2064.1
SCHERLY APPLICATION NUMBER: US/10/650,249
PRIOR APPLICATION NUMBER: US 60/406,657
PRIOR APPLICATION NUMBER: US 60/406,657
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.1
SEQ ID 0.12
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11.7%; Score 888; DB
Best Local Similarity 100.0%; Pred. No. 1.1
Matches 888; Conservative 0; Mismatches
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; ORGANISM: Arabidopsis thaliana
US-10-650-249-12
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US-10-650-249-12
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APPLICANT: Ratcliffe, Oliver
APPLICANT: Ratcliffe, Oliver
APPLICANT: Redde, James
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APPLICANT: Redde, James
APPLICANT: Redde, James
APPLICANT: Pilgin, Marbla L
CURENT FILNG DATE: 2001-04-18
PRIOR APPLICATION NUMBER: 09/937,944
PRIOR PILLING DATE: 2001-08-22
PRIOR FILLING DATE: 2001-10-19
PRIOR FILLING DATE: 2001-11-19
PRIOR FILLING DATE: 2001-11-19
PRIOR FILLING DATE: 2001-12-11
PRIOR APPLICATION NUMBER: 60/336,049
PRIOR FILLING DATE: 2001-12-11
PRIOR PILLING DATE: 2001-12-11
PRIOR FILLING DATE: 2001-12-11
PRIOR FILLING DATE: 2002-06-14
PRIOR FILLING DATE: 2002-06-19
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ORGANISM: Arabidopsis thaliana
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US-10-374-780A-2767
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                               Gaps
                             93;
 Length 795;
                             0; Indels
Query Match
9.1%; Score 692; DB 7; L
Best Local Similarity 89.5%; Pred. No. 5.7e-116;
Matches 795; Conservative 0; Mismatches 0;
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Sequence 2767, Application US/10374780A
Publication No. US20040019927A1
GENERAL INFORMATION:
APPLICANT: Sherman, Bradley K
APPLICANT: Riechmann, Jose Luis
APPLICANT: Jiang, Cai-Zhong
APPLICANT: Heard, Jacqueline E
APPLICANT: Heard, Jacqueline E
APPLICANT: Creelman, Robert A

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Sequence 15, Application US/10650249
Publication No. US20040045055A1
GENERAL INFORMATION:
APPLICANT: Neff, Michael M
TITLE OF INVENTION: THE GENE FOR A DOF TRANSCRIPTION FACTOR CAPABLE OF ALTERING; TITLE OF INVENTION: THE SIZE AND STATURE OF A PLANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TIGGIGCAAICIICAAACGCGIIAIAIAICCAIIACIAGAAGGIAAGGGAGGIGIIAAICAA 4831
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  9.1%;
                         Best Local Similarity 89.5
Matches 795, Conservative
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APPLICANT: MATCLIFFE, Oliver
APPLICANT: RECHMANN, Jose Luis
APPLICANT: RECHMANN, Jose Luis
APPLICANT: RECHMANN, Jose Luis
APPLICANT: BUBEL, Arnold T
APPLICANT: HIGHIN, Marsha L
APPLICANT: PILGRIM, Marsha L
APPLICANT: PILGRIM, Marsha L
APPLICANT: REBERAN, Robert A
APPLICANT: REBERAN, Robert A
APPLICANT: REBERAN, Robert A
APPLICANT: PINEDA, Omaira
APPLICANT: APPLICATION NUMBER: 60/336,049
PRIOR FILING DATE: 2001-08-09
PRIOR FILING DATE: 2001-12-01
PRIOR PILING DATE: 2002-06-14
PRIOR
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Publication No. U920050160493A9
GENERAL INFORMATION:
APPLICANT: Mendel Biotechnology, Inc.
APPLICANT: RATCLIFFE, Oliver
APPLICANT: RATCLIFFE, Oliver
APPLICANT: NIECHMAN, Jose Luis
APPLICANT: DUBELL, Arnold T
APPLICANT: HEARD, Jacqueline E
APPLICANT: JIANG, Cai-Zhong
APPLICANT: REUBER, T. Lynne
APPLICANT: REUBER, T. Lynne
APPLICANT: PINEDA, Omaira
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-225-066A-409
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US-10-225-066A-409
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                                                                                                                                                                       Length 684;
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                                                                                                                                                                   Query Match 9.0%; Score 684; DB 7; Le
Best Local Similarity 100.0%; Pred. No. 1.5e-114;
Matches 684; Conservative 0; Mismatches 0;
FILE REFERENCE: WSHU 2064.1

CURRENT APPLICATION NUMBER: US/10/650,249

CURRENT FILING DATE: 2003-08-28

FRIOR APPLICATION NUMBER: US 60/406,657

PRIOR FILING DATE: 2002-08-02

NUMBER OF SEQ ID NOS: 20

SOFTWARE: PatentIn version 3.1

SOFTWARE: 684
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; ORGANISM: Arabidopsis thaliana
US-10-650-249-15
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RESULT 13
US-10-161-403-90
US-10-161-403-90
Sequence 90, Application US/10161403
Publication No. US20030119104A1
GENERAL INFORMATION:
APPLICANT: Perkins, Edward
APPLICANT: Perkins, Carl

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7265
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8.1%; Score 617.2; DB 6;
Best Local Similarity 93.6%; Pred. No. 7.3e-102;
Matches 659; Conservative 0; Mismatches 33;
APPLICANT: Lindenbaum, Michael
APPLICANT: Greene, Amy
APPLICANT: Leung, Josephine
APPLICANT: Leung, Josephine
APPLICANT: Leung, Josephine
APPLICANT: Stewart, Sandra
APPLICANT: Stewart, Sandra
APPLICANT: Shellard, Joan
TITLE OF INVENTION: CHROMOSOME-BASED PLATFORMS
FILE REPREBENCE: 24601-420
CURRENT FILING DATE: 2002-05-30
CURRENT FILING DATE: 2002-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR PRIOR PLING DATE: 2002-03-21
NUMBER OF SEQ ID NOS: 129
SOFTWARE: RestSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                      LENGTH: 8428
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                                    7146 AGATATCACATCCACTTGCTTTGAAGACGTGGTTGGAACGTCTTTTTCCACGA
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8.1%; Score 617.2; DB 10
Best Local Similarity 93.6%; Pred. No. 7.3e-102;
Matches 659; Conservative 0; Mismatches 33;
                                                                                                                                                                                                                                                                                  APPLICANT: Perez, Carl
APPLICANT: Perez, Carl
APPLICANT: Lindenbaum, Michael
APPLICANT: Lindenbaum, Michael
APPLICANT: Lindenbaum, Michael
APPLICANT: Fleung, Josephine
APPLICANT: Fleung, Josephine
APPLICANT: Fleung, Blena
APPLICANT: Stewart, Sandra
APPLICANT: Shellard, Joan
TITLE OF INVENTION: CHROMOSOME-BASED PLATFORMS
FILT OF INVENTION NUMBER: US/11/006, OT6
CURRENT APPLICATION NUMBER: 60/294, 758
PRIOR FILING DATE: 2001-05-30
PRIOR FILLING DATE: 2001-05-30
PRIOR FILLING DATE: 2001-05-31
NUMBER OF SEQ ID NOS: 129
SEC ID NO 90
SECTUMBER: PASESEQ for Windows Version 4.0
LENGTH: 8428
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; OTHER INFORMATION: pCambia3300 Plasmid
US-11-006-076-90
                                                                                                                                                                                                                                  ; Sequence 90, Application US/11006076; Publication No. US20050181506A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                     US-11-006-076-90
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       7794 CCACCATGTTGGCAAGCTGCTCTAGCCAATACGCAAAACGCCTC 7837
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                                                                                                       Sequence 2, Application US/10161408
; Sequence 2, Application US/10161408
; Publication No. US20040214290A1
; GENERAL INFORMATION:
; APPLICANT: Pabijanski, Steven
; APPLICANT: Pabijanski, Steven
; APPLICANT: Perkins, Edward
; TITLE OF INVENTION: Plant Artificial Chromosomes
; CURRENT APPLICATION UNMERR: US 60/294,687
; PRIOR APPLICATION NUMBER: US 60/294,687
; PRIOR APPLICATION NUMBER: US 60/296,329
; PRIOR APPLICATION NUMBER: US 60/296,329
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2: SEQ ID NOS: 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 8.1%; Score 617.2; DB 8; Best Local Similarity 93.6%; Pred. No. 7.3e-102; Matches 659; Conservative 0; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: pCambia3300 plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Artificial Sequence
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US-10-161-408-2
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                                                                                                                                7468 CCCTCTGGTCTTCTGAGACTGTATCTTTGATATTCTTGGAGTAGACGAGAGTGTCGTGCT 7527 7734 CCCTTTGGTCTTCTAGAGTATTCTTGGAGTAGAGAGTGTCGTGCT 7793
                                          7348 GAIGGCAITIGIAGAAGCCAICTITICTITICTACIGAIGAAGIGACAGAIAG 7407
1614 GAIGGCAITIGIAGGGGCCACCTITICIACITICATICATGAAGIGACAGAIAG 7673
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Search completed: December 31, 2005, 06:23:45 Job time : 3577 secs

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MOLECULE TYPE: synthetic DNA DESCRIPTION: transformation plasmid pPHI1406
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CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATORNEY/AGENT INFORMATION:
NAME: ROCH, MICHAEL J.
REGISTRATION NUMBER: 29,342
REFERENCE/DOCKET NUMBER: 0235
TELEPHONE: (515) 245-3594
INFORMATION FILEPAK: (515) 245-3594
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: double
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US-08-038-768A-1
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                                                                            December 30, 2005, 16:31:40; Search time 840 Seconds (without alignments) 16040.378 Million cell updates/sec
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Sequence 17
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/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
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/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/RE_COMB.seq:*
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Compugen Ltd.
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US-09-011-151-9

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US-09-623-551-17

US-09-810-861B-4

US-09-737-69BB-29

US-09-737-69BB-29

US-10-427-169-29

US-10-427-169-29

US-10-427-169-30

US-10-427-169-30

US-10-427-169-30

US-10-427-180-30

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US-09-027-998A-33
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US-09-441-340-31
US-09-377-466B-23
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US-09-377-466B-15
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                                                                                                                                                                                                                              1303057 seqs, 888780828 residues
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GenCore version
Copyright (c) 1993 - 2005
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Maximum Match 100%
Listing first 45 summaries
                                                   nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Match Length DB
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Patent No. 5569828
GENERAL INFORMATION:
APPLICANT: McMullen, Michael D.; Roth, Bradley A.; Townsend, APPLICANT: Rod
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Rod

TITLE OF INVENTION: MAIZE CHLOROTIC DWARF VIRUS RESISTANCE
NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:
ADDRESSEE: Pioneer Hi-Bred International, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: lowa
STATE: lowa
COUNTRY: United States
ZIP: 50309
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS, Microsoft Windows
SOFEWARE: Microsoft Windows No. 5569828epad
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/038,768A
FTLING DATE: 19930324
                                                                                                                                                                                                                                                                                                                                                                                                                                                 : Pioneer Hi-Bred International, Inc 700 Capital Square, 400 Locust
US-10-232-665-15
US-09-182-117-1
US-09-186-002-16
US-09-186-002-16
US-09-182-117-5
US-09-434-039A-5
US-09-182-117-4
US-09-186-002-14
US-09-186-002-13
US-08-729-601A-43
US-08-729-601A-45
US-09-097-319A-19
US-09-643-971-19
US-09-097-319A-19
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Gaps

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Length 12614;

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4447 GAIGGCATTIGIAGGGCGCCTCCTTTTCTACTGTCCTTTTGATGAAGTGACAGATAG 4388
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                        Score 617.2; DB 3;
Pred. No. 1.9e-110;
0; Mismatches 33;
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US-08-836-402B-7/C
1/US-08-836-402B-7/C
Sequence 7, Application US/08836402B
Patent No. 6063988
GENERAL INFORMATION:
APPLICANT: Rudiger Hain, Regina Fischer
TITLE OF INVENTION: DNA SEQUENCE AND ITS USE
NUMBER OF SEQUENCES:
CORRESSED SEQUENCE ADDRESS:
ADDRESSEE: SPRUNG KRAMER SCHARFER & BRISCOE
                           8.1%;
                                                       Conservative
                                        Similarity
                           Query Match
Best Local Simi
Matches 659;
 US-09-577-424-1
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APPLICANT: Rhoads, David M
TITLE OF INVENTION: METHOD FOR IDENTIFYING COMPONENTS INVOLVED IN SIGNAL
TITLE OF INVENTION: TRANSDUCTION PATHWAYS IN HIGHER PLANTS
FILE REFERENCE: UNL2990
CURRENT APPLICATION NUMBER: US/09/577,424
CURRENT FILING DATE: 2000-05-22
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 12614
                                                                                                                                                                                    1103 AGATATGACATCCACTTGCTTTGAAGACGTGGTTGGAACGTCTTTTTTCCACGA
                                                                                                                           1043 TGCTCCTCGTGGGTGGGGGTCCATCTTTGGGACCACTGTCGGCAGAGGCATCTTGAACGA
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                                                        6868 AGATATCACATCAATCCACTTGCTTTGAAGACGTGGAACGTCTTTTTTCCACGA
                                                                                                               6928 IGTTCCTCGTGGGGGGGTCCATCTTTGGGACCACTGTCGGTAGAGGCATCTTGAACGA
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                              Gaps
                              4 ;
Length 5033;
                             0; Mismatches 30; Indels
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 621; DB 2;
No. 2.8e-111;
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Patent No. 6525245
 8.2%;
             Best Local Similarity 95.1
Matches 653; Conservative
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NAME/KEY: CDS
LOCATION: (1665)..(3317)
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US-09-577-424-1/c
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                                               RESULT 4
US-09-011-151-8/C
US-09-011-151-8/C

Sequence 8, Application US/09011151
Patent No. 6380463
GENERAL INFORMATION:
APPLICANT: Jepson, Ian
TITLE OF INVENTION: DAS CONSTRUCTS
CURRENT APPLICATION NUMBER: US/09/011,151
CURRENT APPLICATION NUMBER: US/09/011,151
CURRENT FILING DATE: 1996-08-02
PRIOR PILING DATE: 1996-08-02
PRIOR FILING DATE: 1995-08-03
NUMBER OF SEQ ID NOS: 33
NUMBER OF SEQ ID NOS: 33
 39 AGCCCTCTGGTCTTCTGAGAC 19
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; OTHER INFORMATION: Plasmid pMJB1
US-09-011-151-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           279 TGCTTTGAAGACGTGGTTGGAACGTCTTCTTTTTCCACGATGTTCCTCGTGGGGGGT
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97.7%; Pred. No. 4.6e-100;
                             CURRENT ARE:

APPLICATION NUMBER: US/08/836,402B
FILING DATE: 02-SEP-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 44 40 200.7 (Germany)
FILING DATE: 10-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Kurf G. Briscoe
REGISTRATION NUMBER: 33,141
REGISTRATION NUMBER: 33,141
REFERENCE/DOCKET NUMBER: Bayer 9840-KGB
TELEPHONE: (914) 332-1700
TELEPHONE: (914) 332-1904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6788 AGCCTCTGGTCTTCTGAGAC 6808
                 Microsoft Windows 98
                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2728 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 97.73
Matches 607; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-836-402B-7
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Sequence 17, Application US/09623551

Sequence 17, Application US/09623551

Patent No. 6774281

GENERAL INFORMATION:

APPLICANT: Stuiver, Maarten

APPLICANT: Custers, Jerome

APPLICANT: Simons, Lambertus

TITLE OF INVENTION: Plants

TITLE OF INVENTION: Plants

TITLE OF INVENTION: Plants

FILE REFERENCE: MOG57706(UST

CURRENT FILING DATE: 2000-11-15

PRIOR PPLICATION NUMBER: EP 98104076.9

PRIOR FILING DATE: 1998-03-06

PRIOR FILING DATE: 1999-03-08

NUMBER OF SEQ ID NOS: 29

SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5310 TAGCCTTTCCTTTATCGCAATGATGGCCATTTGTAGAAGCCATCTTCCTTTTCTACTGTCC 6369
986 AGCTGGGCAATGGAATCCGAGGAGGTTTCCGGATATTACCCTTTGTTGAAAAGTCTCAAT 1045
                                                            1046 IGCCCTTGGTCTTCTGAGACTGTATCTTTGGAGTAGTAGTAGTAGACAAGTGTCTCGTG 1105
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                                   6788 AGCCCTCTGGTCTTCTGAGACTGTATCTTTGATATTCTTGGAGTGACGAGAGTGTCGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Description of Artificial Sequence:Combination; OTHER INFORMATION: 35S Promoter with the Glucanase II leader US-09-623-551-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 907;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 462.2; DB 3;
Pred. No. 1.4e-80;
0; Mismatches 43;
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illarity 80.4%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                     6848 CICCACCATGITG 6860
                                                                                                                            1106 CTCCACCATGTTG 1118
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                                                                                                                                                                                     RESULT 6
US-09-623-551-17/c
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        93 TGCCCTTTGGTCTTCTGAGACTGTATCTTTGATATTTTTGGAGTAGACAAGTGTCGTG 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 7.3%; Score 554.2; DB 3; Best Local Similarity 92.3%; Pred. No. 1.9e-98; Matches 621; Conservative 0; Mismatches 38;
                                                                                                                                                                                    GENERAL INFORMATION:

APPLICANT: Jepson, lan
TITLE OF INVENTION:
FILE REFERENCE: PPD 50059/UST
CURRENT APPLICATION NUMBER: US/09/011,151
CURRENT FILING DATE: 1998-01-29
PRIOR APPLICATION NUMBER: PCT/GB96/01883
PRIOR PLING DATE: 1996-08-02
PRIOR FILING DATE: 1995-08-03
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATENTLY NOS: 33
SOFTWARE: PATENTLY VERSION 3.0
                                                                                                                                                     Sequence 9, Application US/09011151
Patent No. 6380463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Plasmid pMJB1
US-09-011-151-9
                                           6860
                                                                        21
                                                                           CTCCACCATGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1138
                                                                                                                          RESULT 5
US-09-011-151-9
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US-09-810-861B-4/C

US-09-810-861B-4/C

Sequence 4, Application US/09810861B

Patent No. 6770799

GENERAL INFORMATION:

APPLICANT: Mor. Teafrir S.

APPLICANT: Mor. Teafrir S.

APPLICANT: Arntzen, Charles J.

APPLICANT: Macon, Hugh S.

TITLE OF INVENTION: EXPRESSION OF RECOMBINANT HUMAN ACETYLCHOLINESTERASE IN

TITLE OF INVENTION: EXPRESSION OF RECOMBINANT HUMAN ACETYLCHOLINESTERASE IN

TITLE OF INVENTION: EXPRESSION OF RECOMBINANT HUMAN ACETYLCHOLINESTERASE IN

TITLE OF INVENTION: EXPRESSION OF RECOMBINANT HUMAN ACETYLCHOLINESTERASE IN

TITLE OF INVENTION: EXPRESSION OF RECOMBINANT HUMAN ACETYLCHOLINESTERASE IN

TITLE OF INVENTION: EXPRESSION OF RECOMBINANT HUMAN ACETYLCHOLINESTERASE IN

TITLE OF INVENTION: EXPRESSION OF RECOMBINANT HUMAN ACETYLCHOLINESTERASE IN

TITLE OF INVENTION: EXPRESSION OF RECOMBINANT HUMAN ACETYLCHOLINESTERASE IN

TITLE OF INVENTION: 105/09/810,861B

CURRENT FILING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: 60/190,440

PRIOR APPLICATION NUMBER: 60/190,440

PRIOR APPLICATION NUMBER: 2001-03-17

NUMBER OF SEQ ID NOS: 5

SOFTWARE: PARAMETER PARAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PEATURE:
NAME/KRY: misc feature
LOCATION: (11862)..(12157)
OTHER INFORMATION: Description of Artificial Sequence: plasmid vector
OTHER INFORMATION: pTM036. Identity of sequence residues 11862-12157 unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATAGCCTTTCCTTTATCGCAATGATGGCATTGTAGAAGCCATCTTCCTTTTCTACTGTC 6368
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                                                                                                                                                                                                                                                                                                                                                    6668 ATGATGGCATTTGTAGAAGCCATCTTCCTTTCTACTGTCCTTTCGATGAAGTGACAGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92 AGCCCTCTGGTCTTCTGAGACTGTATCTTTGATATTCTTGGAGTAGACGAGTGTCGTG
                                                        -----TATCACATCAATCCACT
                                                                                                                                                                                                                                           AGCCCTCTGGTCTTCTGAGACTGTATCTTTGATATTCTTGGAGTAGACGAGAGTGTCGTG
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                      GAGTAGACGAGAGTGTCGTGCTCCACCATGTTGGGGATCTAGATATCACATCCACT
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Best Local Similarity
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APPLICANT: Morey Teafrir S.
APPLICANT: Soreq, Hermona
APPLICANT: Soreq, Hermona
APPLICANT: ARTIZEO;
TITLE OF INVENTION: EXPRESSION OF RECOMBINANT HUMAN ACETYLCHOLINESTERASE IN
TITLE OF INVENTION: TRANSGENIC PLANTS
FILE REFERENCE: BTI-45
CURRENT PILING DATE: 2001-03-16
FRICK APPLICATION NUMBER: 60/190,440
PRIOR FILING DATE: 2000-03-17
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Ver. 3.1
SEQ ID NO 3
LENGTH: 5767
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            544
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346 ITTGAATCTTTGACTCCATGCGGAATTATCACATCAATCCACTTGCTTTGAAGACGTGGT
                                                                                  603 AGATATCACATCAATCCACTTGCTTTGAAGACGTGGGTTGGGAACGTCTTTTTTCCACGA
                                                     6566 TGGAACGTCTTCTTTTCCACGATGTTCCTCGTGGGTGGGGGTCCATCTTTGGGACCACT
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US-09-810-861B-3
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Best Local Similarity 86.5%; Pred. No. 3.9e-80;
Matches 582; Conservative 0; Mismatches 0.
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; Sequence 3, Application US/09810861B
; Patent No. 6770799
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Gaps

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LOCATION: (1)..(1800)
OTHER INFORMATION: y = t/u or c
OTHER INFORMATION: chimeric promoter fusion CaMV and Act8 polynucleotides +
OTHER INFORMATION: tro
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                                                                                                                   TGAACGATAGCCTTTTATCGCAATGATGGCATTTGTAGAAGCCATCTTCCTTTTCT
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Sequence 29, Application US/09737626A

GENERAL INFORMATION:
APPLICANT: Flacinski, Stanislaw
APPLICANT: Flacinski, Stanislaw
APPLICANT: Wilkinson, Jack
TITLE OF INVENTION: No. 6660911e1 Plant Expression Constructs
TITLE OF INVENTION: NO. 6660911e1 Plant Expression Constructs
CURRENT FILING DATE: 2002-02-25
PRIOR PLLING DATE: 2002-02-25
PRIOR PLLING DATE: 2000-12-15
NUMBER OF SEQ ID NOS: 30

SOFTWARE: PatentIn version 3.0
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Pred. No. 1.8e-64;
0; Mismatches 37;
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Best Local Similarity 81.1%;
Matches 489; Conservative
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US-09-737-626A-29/c
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NAME/KEY: promoter
LOCATION: (1)..(1800)
OTHER INFORMATION: y = t/u or c
OTHER INFORMATION: chimeric promoter fusion CaMV and Act8 polynucleotides + Act8
OTHER INFORMATION: tro
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APPLICANT: Fincher, Karen
APPLICANT: Fincher, Karen
APPLICANT: Wilkinson, Jack
TITLE OF INVENTION: No. 646228el Plant Expression Constructs
FILE REFERENCE: 38-21(51499)C
CURRENT APPLICATION NUMBER: US/09/737,698B
CURRENT FILING DATE: 2000-12-15
PRIOR APPLICATION NUMBER: US 60/171,173
PRIOR PELING DATE: 1999-12-16
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin version 3.0
SEQ ID NO 29
LENGTH: 1800
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; Sequence 29, Application US/09737698B
; Patent No. 6462288
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j Sequence 29, Application US/10427180

j Patent No. 649696

j Patent No. 6496966

j CENERAL INFORMATION:

j APPLICANT: Fincher, Karen

j APPLICANT: Fincher, Stanislaw

j APPLICANT: Fincher, Stanislaw

j APPLICANT: Wilkinson, Jack

j TITLE OF INVERTION: No. 694669681 Plant Expression Constructs

j TITLE OF INVERTION: No. 694669681 Plant Expression Constructs

j CURRENT APPLICATION NUMBER: US/10/427,180

j CURRENT APPLICATION NUMBER: US/09/737,626A

pRIOR FILING DATE: 2002-02-25

pRIOR FILING DATE: 2002-02-25

j NUMBER OF SEQ ID NOS: 30

j SOFTWARE: PatentIn version 3.0
                                                                                                                                        : 77
                                                                                 DB 3; Length 1800;
                                                                                                                                        Indels
                                                                              Score 379.8; DB 3;
Pred. No. 1.8e-64;
0; Mismatches 37;
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                                                                                    5.0%;
                                                                                                            Best Local Similarity 81.1 Matches 489; Conservative
; OTHER INFORMATION: tro
US-10-427-169-29
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LENGTH: 1800
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NAME/KEY: promoter
LOCATION: (1)..(1800)
OTHER INFORMATION: y = t/u or c
OTHER INFORMATION: chimeric promoter fusion CaMV and Act8 polynucleotides + Act8
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                                                            535 GGAAGCTTGATATCACATCAATCCACTTGCTTTGAAGACGTGGTTGGAACGTCTTCTTTT
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i Sequence 29, Application US/10427169

sequence 29, Application US/10427169

parent No. 6919495

i GENERAL INPORMATION:

APPLICANT: Fincher, Karen

APPLICANT: Flasinski, Stanislaw

APPLICANT: Flasinski, Stanislaw

TITLE OF INVENTION: No. 6919495el Plant Expression Constructs

TITLE OF INVENTION NUMBER: US/10/427,169

CURRENT FILING DATE: 2003-05-01

PRIOR APPLICATION NUMBER: US/09/737,626

PRIOR APPLICATION NUMBER: 09/737,626

PRIOR APPLICATION NUMBER: 09/737,626

PRIOR APPLICATION NUMBER: 09/737,626

SEQ ID NOS: 30

SOFTWARE: PatentIn version 3.0

SEQ ID NO 29

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Act2 in

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EQ ID NO 30
LENGTH: 1742
TYPE: DNA
ORGANISM: artificial sequence
FRATURE:
NAWE/KEY: promoter
LOCATION: (1)..(1742)
OTHER INFORMATION: chimeric promoter fusion CaMV and Act2 polynucleotides +
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Patent No. 6660911
GENERAL INFORMATION:
APPLICANT: Flasinski, Stanislaw
APPLICANT: Flasinski, Stanislaw
APPLICANT: Wilkinson, Jack
TITLE OF INVENTION: No. 6660911e1
FILE REFERENCE: 38-21(51499) B
CURRENT APPLICATION NUMBER: US/09/737,626A
CURRENT FILING DATE: 2002-02-25
FRIOR APPLICATION NUMBER: 09/737,626
                                                                                                                                                                        Query Match 5.0%; Score 379.2; DB 3; Length Best Local Similarity 81.0%; Pred. No. 2.4e-64; Matches 489; Conservative 0; Mismatches 38; Indels
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APPLICANT: Fincher, Karen
APPLICANT: Fincher, Karen
APPLICANT: Wilkinson, Jack
TITLE OF INVENTION: No. 6462258el Plant Expression Constructs
FILE REFERENCE: 38-21(51499)C
CURRENT APPLICATION NUMBER: US 60/171,173
PRIOR APPLICATION NUMBER: US 60/171,173
PRIOR FILING DATE: 1999-12-16
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.0
                                                                                                                                              Query Match 5.0%; Score 379.8; DB 3; Length Best Local Similarity 81.1%; Pred. No. 1.8e-64; Matches 489; Conservative 0; Mismatches 37; Indels
        CRGANISM: artificial sequence

FEATURE:

NAME/KEY: promoter

LOCATION: (1)..(1800)

OTHER INFORMATION: y = t/u or c

OTHER INFORMATION: chimeric promoter fusion CaMV is OTHER INFORMATION: tro

US-10-427-180-29
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    ORGANISM: artificial sequence
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ORGANISM: artificial sequence
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NAME/KEY: promoter
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                                                          TYPE: DNA ORGANISM: artificial sequence FEATURE: NAME/KEY: promoter NAME/KEY: promoter LOCATION: (1)..(1742) OTHER INFORMATION: chimeric promoter fusion CaMV and Act2 polynucleotides + OTHER INFORMATION: tro
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PRIOR FILING DATE: 2000-12-15
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.0
SEQ ID NO 30
LENGTH: 1742
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OTHER INFORMATION: chimeric promoter fusion CaMV and Act2 polynucleotides
OTHER INFORMATION: tro
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5.0%; Score 379.2; DB 3; Length 1742;
Best Local Similarity 81.0%; Pred. No. 2.4e-64;
Matches 489; Conservative 0; Mismatches 38; Indels 77;
CURRENT APPLICATION NUMBER: US/10/427,169
CURRENT FILING DATE: 2003-05-01
FRIOR APPLICATION NUMBER: US/09/737,626A
FRIOR FILING DATE: 2002-02-25
FRIOR PILING DATE: 2000-12-15
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin version 3.0
SEQ ID NO 30
LENGTH: 1742
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CK438362 GQ0083.BR CK43832 GQ0083.BR CC472761 GQ0081.BR AA565745 28394 Lam AQ361936 mgxb0005M AQ362115 mgxb0003F CK437874 GQ042.BR CK437874 GQ042.BR CK99882 WiscDBLOx CW998169 GQ0165.B7

CV961115 PYPCY 10 CV965337 PYPCY 99 CV965230 PYPCY 99 CV96495 PYPCY 10 BZ586494 3590 1 18 BZ586497 3590 1 18 BZ586953 3590 1 18 CZ908574 4018066E1 CG805032 1118056E1

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BH753412 SALK 0288 BH212594 SALK 0077 BH171104 SALK 0037 BH619277 SALK 0407

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Direct Submission

L Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
The sequences are based on single pass reads.
Life Technologies (a division of Invitrogen) members carried out
full-length librairies construction : Temple G.
Genoscope members carried out sequencing and annotation : Castelli
V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C.,
Schachter V., Weissenbach J., Salanoubat M.
URGV INRA : Clepet C., Caboche M.
Annotation is based on the June 2003 version of the Arabidopsis
genome released by MIPS (Munich Information center for Protein
Sequences). 5 prime and 3 prime are assembled with Phrap.
http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full
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Arabidopsis thailana
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AL084743 Arabidops
CG729372 1119111D0
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Copyright (c) 1993 - 2005 Compugen Ltd.
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rosida; eurosida II; Brassicales; Brassicaceae; Arabidopsis.

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Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V.,
Temple, G., Caboche, M., Weissenbach, J. and Salanoubat, M.
Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:
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Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :

Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)

- Web : www.genoscope.cns.fr)

The sequences are based on single pass reads.

Life Technologies (a division of Invitrogen) members carried out full-length librairies construction : Temple G.

Genoscope members carried out sequencing and annotation : Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.

URGY INRA : Clepet C., Caboche M.

Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences) : 5 prime and 3 prime are assembled with Phrap.
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                                                                                                                                                                                   Length 1466;
                                                                                                                                                                                                                          1;
                                                                                                                                                                                   DB 4;
                                                                                                                                                                                   16.6%; Score 1256.4; DB 4
.larity 99.1%; Pred. No. 3.6e-213;
Conservative 0; Mismatches 11;
                                           "abud
  /db_xref="taxon:3702"
/clone="GSLTRB522B04"
/tissue_type="Flowers and bu/ecotype="Col-0"
/plasmid="pcMvSpORT_6"
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/gene="At3g55370"
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BX824803.1 GI:42464248
HTC; GSLT CDNA.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

E (bases 1 to 1320)
Menard,M., Aury,J.M., Jaillon,O., Wincker,P., Clepet,C., Menard,M., Cruaud,C., Quetier,F., Scarpelli,C., Schachter,V., Temple,G., Caboche,M., Weissenbach,J. and Salanoubat,M.
Whole Genome Sequence Comparisons and 'Pull-Length' cDNA Sequences:
A Combined Approach to Evaluate and Improve Arabidopsis Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana Full-length cDNA Complete sequence from clone GSLTPGH73ZF02 of Hormone Treated Callus of strain col-0 of Arabidopsis thaliana (thale cress).
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                             CAGCACTAGCTATTCTTGATGATTCTTTGTTGGTTGGGGGTGTACATTGGTGCTTGTCAT
           TITGGGTAATATCAACATAAACTCAGGCAGGAACGAGGAATACACATCATGGGGAGGTAA
                                                                   CAGITCITGGACCGGITTCACCTCCAACAACTCAACAGGCCATCTCTAAGTACT
                                                                                     CAGCACTAGCTATTCTTGATTCTTTTGTTGGTTGGGGTGTACATTGGTGCTTGTCAT
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Best Local Similarity 92.9%; Pred. No. 1.5e-188;
Matches 1221; Conservative 0; Mismatches 0;
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/mol_type="mRNA"
/db_xref="taxon:3702"
/clone="GSLTFB52ZB03"
/tissue_type="Flowers and bu /ecotype="Col-0"
/plasmid="pcMVSPORT_6"
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5184 1137 Direct Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage: Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage: Bp 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web: www.genoscope.cns.fr)

The sequences are based on single pass reads.

Life Technologies (a division of Invitrogen) members carried out full-length librairies construction : Temple G.

Genoscope members carried out sequencing and annotation : Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.

URGV INRA : Clepet C., Caboche M.

Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap.

http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full _rengin http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis. Location/Qualifiers 1. .1320

```
Arabidopsis
Unpublished (2004)
Contact: Woody ST
Biotechnology Center
University of Wisconsin-Madison
425 Henry Mall, Madison, WI 53706, US
Tal: (608) 262-4640
Email: swoody@facstaff.wisc.edu
Class: TAIL-PCR.
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                                               Callus
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Pred. No. 2.9e-161;
0; Mismatches 92;
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                                  /clone="GSLTPGH73ZF02"
/tissue_type="Hormone Treated
/ecotype="Col-0"
                                                                 /plasmid="pCMVSPORT_6"
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/gene="At3g55370"
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sequences"
/note="Vector: pDS-Lox; Sequence generated in the course
/note="Vector" pDS-Lox; Sequence generated in the course
for an Arabidopsis T-DNA tagging program. TAIL-PCR was used
to generate sequencing templates that represent A.t.
genomic DNA flanking the left border of the pDs-Lox T-DNA
insert. PCR products were sequenced directly by using the 5184 5244 5364 5424 1320 5124 CW802337 136 bp DNA linear GSS 23-NOV-2004 WiscDBLox477-480J24 Arabidopsis thaliana T-DNA insertion flanking sequences Arabidopsis thaliana genomic, genomic survey sequence. Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Wagnoliophyta; eudicotyledons; core eudicotyledons;
roside; euroside II; Brassicales; Brassicaceae; Arabidopsis.

(bases 1 to 736)
Woody, S.T., Monson, S.S., Jester, P.J., Austin-Phillips, S.,
Amasino, R.M., Sussman, M.R. and Krysan, P.J.
A New Community Resource for Knocking-Out Small Genes and
Tandemly-Duplicated Gene Families and for Mosaic Analysis in /clone_lib="Arabidopsis thaliana T-DNA insertion flanking 842 AGAGAATGATCAGGATCGGGGTAGGGATGGGGATGGAGTGAATAACTTATCAAGAAACTC 901 primary (Basta-resistant) 1021 CAGAACTAGCTATTCTTGATCACTCTCCTGTCCGTTGGGGGTGTACATTGGTGCTTCTCAT 1141 TCAAAGGAAAGGTATGGTCATAACACTATCTCCTTGATCTCCCAAAAGATGTCTTCAAAGG 1201 TGAGTATGTTTATTGGTTGGCTTCTGGTCATATTTATGTCTTATTAGAATTTGGTCTTAT CAGTICTIGGACCGGITTICACCICCAACAACICAACAGGCCAICTCTCATICTAAGIACI CAGCACTAGCTATTCTTGATGATTCTTTTGTTGGTTGGGGTGTACATTGGTGCTTGTCAT 1081 GCGAGTCATCGCTGAGGAAGATCAAACCATGCAGCTATATCCAAAGGCTAATCTTGAGGC TCAAAGGAAAGGTATGGTTATAAAACTATCTTTTGATCTTTTAAAAGATCTTCAAAGTG TGAGTATGTTTATTGGTTGGCTTCTGGTGATATTTATGTTTTAGAATTTGGTCTTAT GCGAGTTATTGCTGAGGAAGATCAAACCATGCAGCTATATCCAAAGGCTAATTTTGAGGC 1. 736 /organism="Arabidopsis thaliana" /mol type="genomic DNA" /cultivar="Col-O ecctype" /db_xref="taxon:3702" /tissue_type="seeds produced by transformants" usa

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/note="Vector: pDS-Lox; Sequence generated in the course of an Arabidopsis T-DNA tagging program. TAIL-PCR was used to generate sequencing templates that represent A.t. genomic DNA flanking the left border of the pDs-Lox T-DNA insert. PCR products were sequenced directly by using the p745 primer 5' AACGTCCGCAATGTGTTATTAAGTTGTC 3'"
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                                                                                                                                                                                                                                                                                                                                                                                   (Basta-resistant)
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1 (bases 1 to 720)
Mody, S.T., Monson, S.S., Jester, P.J., Austin-Phillips, S., Amsino, R.M., Sussann, M.R. and Krysan, P.J.
A New Community Resource for Knocking-Out Small Genes and Tandemly-Duplicated Gene Families and for Mosaic Analysis
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100.0%; Pred. No. 4.3e-116;
ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                      organism="Arabidopsis thaliana"
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                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="seeds produced transformants"
                                                                                                                               Contact: Woody ST
Biotechnology Center
University of Wisconsin-Madison
425 Henry Mall, Madison, WI 53706, UK
Tel: (608) 262-4640
Email: swoody@facstaff.wisc.edu
Class: TAIL-PCR.
                                                                                                                                                                                                                                                                                                                      /mol_type="genomic_DNA"
/cultivar="Col-O ecotype"
/db_xref="taxon:3702"
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Unpublished (2004)
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Arabidopsis thaliana
Bukaryota, Viridiplantaes, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                       TINANNIVININAACTITICCGCCTTTCGTGAAAAAATGCGCATGTTCTTGTTGGAATCTAG
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                                                       Score 720.4; DB 10;
Pred. No. 9.2e-118;
0; Mismatches 12;
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Best Local Similarity 98.4%;
Matches 724; Conservative
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VERSION
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Matches 792; Conservative
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Par Ares, Costantino, Vittorioso, Davies, Gilmartin, Giraudat, Parcy, Sablowski, Coupland, Martin, Angenent, Baeumlein, Carbonero, Colombo, Tonelli, Engercen, Droege-Least, Gatz, Kavanagh, Kushnir, Zabeau, Laux, Holdsworth Ruberti, Smeekens, Somssich, Weisshaar, Traas
Bielefeld University, Institute for Genome Research Universitestestasse 25, D-3354 Bielefeld, Germany
Finalation: no full cas detected
Agi: Ar3655370; SeqAnalysis: truncated in 5' at pos 179;
Translation: no full cas detected
Agi: Ar3655370; SeqAnalysis: truncated in 5' at pos 179;
Translation: no full cas detected
Agi: Ar3655370; SeqAnalysis: truncated in 5' at pos 179;
Translation: no full cas detected
Agi: Ar3655370; SeqAnalysis: truncated in 5' at pos 179;
Translation: no full cas detected
Agi: Ar3655370; SeqAnalysis: truncated in 5' at pos 179;
Translation: no full cas detected
GC Coupland (coupland-ad-miproment and physiological
performance), a Trilateral Co-Operation in Plant Genomics between
Spain (McY7), France (GENOPLANTE) and Germany (GABI) coordinated by
G. Coupland (coupland-ad-mipiz-keeln.myg.de). Authors: Vincent
Thareau (IBP-Orsay UMR8618 CNRS-UPS, thareau-ad-ibp.u-psud.fr) and
Alain Lecharny (MCKV-Exry UMR INRA-CNRS-UBVE,
Lecharny ad-ibp.u-psud.fr).
Definition of the terms used to describe the quality of the clone:
The about 2550 sequences from the clone collection were sorted
according to clones and clustered. If more than one contig was
formed, the clone was designated 'Contemination'. The contigs and
singletons were blasted against CDS plus pseudogenes from the
TIGRV5 annotation, and the resulting AGI code is presented if more
than 90 percent identity was found. The sequences or contigs for which
against all TIGRV5 introns, and matches longer than 50 percent identity
against all TIGRV5 protein sequences was performed. Full good: better than 95 percent of the sequences
to be percent identity; full good: better than 95 percent of the sequence;
weak similarity: less than 95 percent of the sequence;
                                                                                                                                                                                                                                                                                                                                                                                                             DR750042
79-L021445-065-006-G10-SeLB MPIZ-ADIS-065d Arabidopsis thaliana
CDNA clone 006-G10, mRNA sequence.
                                                                                              5335
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REGIA, an EU project on functional genomics of transcription factors from Arabidopsis thaliana

Comp. Funct. Genomics 3 (2), 102-108 (2002)
670 ATTTANGTTTTATAGAATTTGGTCTTATATATATTGCTTATATAGAGGTG 720
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Arabidopsis thaliana
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TITLE

COMMENT

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/lab hose Tool DHSalpha"
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/note=Tvector: pDONR201; In the context of the EU-funded project REGIA (QLG-CT11999-00876, coordinator Javier Paz-Ares), a Set of transcription factor ORFs was generated. The ORFs were produced in a decentralized way in the labs of the participants. Most of the ORFs were generated by RT-PCR using CDNA from various A. thaliana tissues as a template. Initially, it was planned to use yeast recombination to move the ORFs from the cloning vectors into target constructs. For this reason, a number of the clones contein 'REGIA tags' (RG_tagl: Spr-AATTCCCACCACCACC-3pr; RG_tagl: During the lifetime of the Spr-CATGGCAATTCCCGGGATC-3pr; During the lifetime of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          project, the GATEWAY system became available and finally all ORFs were transferred into GATEWAY vectors. At the end of the REGIA project, the clones were collected as plasmid DNA. For end-sequencing at the DNA core facility of the MPI of Plant Breeding Research (ADIS, head: Bernd Weisshaar), the plasmids were re-transformed into MPISALPha, arrayed into 96 well plates and new plasmid DNA was prepared. Re-transformation proved to be difficult because a number of clones displayed poor growth. Data submission has been handled by GabiPD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4533 ACCCTAGCAAGTITCATAGCTACGGTCAAAICCCGGAGTTTAATICCAACTIGCCCAICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                       Obviously, information about these clones is missing in the submitted data.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 688.4; DB 8;
Pred. No. 4.5e-112;
0; Mismatches 1;
                                                                                                                                         insert Length: 972 Std Brror: 0.00 Seg primer: SelB GTAACATCAGAGATTTTGAGACAC. Location/Qualifiers
                                                                                                                                                                                                                                                                            'organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (http://gabi.rzpd.de)."
                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/ecotype="Columbia"
/db_xref="GABI:1452133"
                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:3702"
/clone="006-G10"
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셤 ઠે 요 ò g ò 셤 ઠે 셤 ò 셤 8 셤 ð

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lecharny-adibb...paudiff)

Definition of the terms used to describe the quality of the clone:
The about 220 sequences from the clone collection were sorted
according to clones and clustered. If more than one contig was
singletons were blasted against Contamination. The contigs and
singletons were blasted against CDS plus pseudogenes from the
TIGRYS annotation, and the resulting AdI code is presented if more
than 90 percent identity was found. The sequences were also blasted
against all TIGRYS introns, and matches longer than 50 bp with 95
percent identity are reported as 'intron found'. The remaining
terms for SeqAnalysis describe the outcome of the evaluation of the
CDS defected after pairwise alignment with CDS plus pseudogenes
from the TIGRYS protein sequences or contigs for which
a full CDS with or without STOP codon was detected, a BLASTp
against all TIGRYS protein sequences was performed. Full perfect:
100 percent identity, full good: better than 95 percent identity
over more than 95 percent of the sequence; partial good: better
than 95 percent identity over less than 95 percent identity
weak similarity: less than 95 percent identity
weak similarity: less than 95 percent identity
weak similarity: less than 95 percent of the sequence;
better that the collection contains a few clones for which sequencing was
not successful, which could have simple technical reasons.
Obviously, information about these clones is missing in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone=1006-G10"
//lab host==8.006-G10"
//lab host==8.006-G10"
/clone_lib="MpIZ-ADIS-065d"
//clone_lib="MpIZ-ADIS-065d"
//clone_lib="MpIZ-ADIS-065d"
//clone=Tweetcr: pDOMR201; In the context of the EU-funded project REGIA (QLG-TIL1999-00876, coordinator Javier Paz-Ares), a set of transcription factor ORFs was generated. The ORFs were produced in a decentralized way in the labs of the participants. Most of the ORFs were generated by RT-PCR using cDNA from various A. thaliana tissues as a template. Initially, it was planned to use yeast recombination to move the ORFs from the cloning vectors into target constructs. For this reason, a number of the clones contain 'REGIA tags' (RG_tag1:
5pr-AATCCAGCTCACCACC-3pr; RG_tag2:
5pr-AATCAGCAATTCCAGCACT-3pr; RG_tag2:
5pr-AATCAGCAATTCCAGCACT-3pr; RG_tag2:
5pr-AATCAGCAATTCCAGCACT-3pr; RG_tag2:
5pr-AATCAGCAATTCCAGCACC-3pr; RG_tag2:
5pr-AATCAGCAATTCCAGCACT-3pr; RG_tag2:
5pr-AATCAGCAATTCCAGCAT-3pr; RG_tag2:
5pr-AATCAGCAATTCCAGCAT-3pr; RG_tag2:
5pr-AATCAGCAATTCCAGCAT-3pr; RG_tag2:
5pr-AATCAGCAATTCCAGCAT-3pr; RG_tag2:
5pr-AATCAGCAATTCCAGCAT-3pr; RG_tag2:
5pr-AATCAGCAATTCCAGCAT-3pr; RG_tag2:
5pr-AATCAGCAATTCAGCAGAT-3pr; RG_tag2:
5pr-AATCAGCAATTCAGCAGAT-3pr; RG_tag2:
5pr-AATCAGCAATTCAGCAGAT-3pr; RG_tag2:
5pr-AATCAGCAATTCAGCAGAT-3pr; RG_tag2:
5pr-AATCAGCAGT-3pr; RG_tag2:
5pr-AATCAGCAGT-3pr; RG_tag2:
5pr-AATCAGCAGT-3pr; RG_tag2:
5pr-AATCAGCAGT-3pr; RG_tag2:
5pr-AATCAGCAGT-3pr; RG_tag2:
5pr-AATCAGCAGT-3pr; RG_tag2:
5pr
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(coupland-ad-mpiz-koeln.mpg.de). Authors: Vincent
-Orsay UMR8618 CNRS-UPS, thareau-ad-ibp.u-psud.fr) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4233 TGGTGGAACGTGCTCGGATCGCAAAAGTCCCATTGCCTGAAGCAGCTCTAAATTGCCCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
    G. Coupland (coupland-ad-mpiz-koeln.mpg.de)...
Thareau (IBP-Orsay UMR8618 CNRS-UPS, thareau-Alain Lecharny (URGV-Evry UMR INRA-CNRS-UEVE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seq primer: Sela TCGCGTTAACGCTAGCATGGATCTC.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8.9%; Score 672.2; DB 8;
88.8%; Pred. No. 3.5e-109;
ive 0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Arabidopsis thaliana"
/mol_type="mRNA"
/ecotype="Columbia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="GABI:1452143"
/db_xref="taxon:3702"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Insert Length: 868 Std Error:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         clone="006-G10"
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Matches 78
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Bielefeld University, Institute for Genome Research
Universitaetsstrasse 25, D-33594 Bielefeld, Germany
Email: bernd.weisshaar@uni-bielefeld.de
AGI: AT3G55370; SeqAnalysis: truncated in 5' at pos 179;
Translation: no full cds detected
Data analysis performed in the frame of REGULATORS (Exploiting
inter-species conservation in promoter sequences to identify
regulators of reproductive development and physicological
performance), a Trilateral Co-Operation in Plant Genomics between
Spain (MCyT), France (GENOPLANTE) and Germany (GABI) coordinated by
                                                                                                                                                                                                           4772
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DR749973 868 bp mRNA linear EST 19-JUL-2005
                                                                                                                                                                                                                                                                                                                                                                            TGGTGCAATCTTCAAACGCGTTATATCCATTACTAGAAGGTAAGGGAGGTGTTAATCAAG 4832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1833 GTGATTCTCAACAGAAGAGTAGTGATTATTCCAATCAGCTAATGTTTAAGCCCTTGATGG 4892
                                                                                                                                                                                                                                                                                              349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               201 ATATCAACATAAACTCAGGCAGGAACGAGGAATACACATCATGGGGAGGTAACAGTTCTT 142
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REGIA, an EU project on functional genomics of transcription factors from Arabidopsis thaliana
Comp. Funct. Genomics 3 (2), 102-108 (2002)
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
1 (bases 1 to 868)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4953 ATCAGGATCGGGGTAGGGATGGGGATGAGTGAATAACTTATCAAGAAACTTTTTGGGTA
                                                                                      468 GAACTCAAATAAGCAACATGATAAGTGGTATGAGTTCTAGTGGGGGATCTTGGATGCAT
                                                                                                                                                                                                                GGAGAATACCTCCATCACAACAACTCAGCAATTCCCTTTGATCAACACTACCGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     311 ------AGGCGGGGTTAGCGCCACGCAAACAAATGTGAAGGCGGGAAGAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 261 ATCAGGATCGGGGTAGGGATGGGATGGAGTGAATAACTTATCAAGAAACTTTTTGGTA
                                                                                                                                                                                                                                                                                         408 GGAGAATACCTCCATCACAACAAGCTCAGCAATTCCCTTTCTTGATCAACACTACCGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                           1893 ATTTTTCAGGCGGGGTTAGCGCCACGCAACAAGAAATGTGAAGGCGGGAAGAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5013 ATATCAACATAAACTCAGGCAGGAACGAGGAATACACATCATGGGGAGGTAACAGTTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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DR749973
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                                                                                                                                                                                                                4713
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AUTHORS
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KEYWORDS
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Carbonero, P., Colombo, L., Tonelli, C., Engstroem, P., Droege-Laser, W., Gatz, C., Kavanagh, T., Kushnir, S., Zabeau, M., Laux, T., Hordsworth, M., Ruberti, I., Ratcliff, F., Smeekens, S., Somssich, I., Weisshaar, B. and Traas, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Insert Length: 866 Std Error: 0.00
Seg primer: SeLA TCGCGTTAACGCTAGCATGGATCTC.
Location/Qualifiers
                                                                                                                          factors from Arabidopsis thaliana
Comp. Funct. Genomics 3 (2), 102-108 (2002)
                                                                                                                                                                                                                                                                        Ruberti, Smeekens, Somssich, Weisshaar, Traas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Arabidopsis thaliana"
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/ecotype="Columbia"
/db_xref="GABI:1452132"
/db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lecharny-ad-ibp.u-psud.fr).
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79-L021444-065-006-G10-SeLA MPIZ-ADIS-065d Arabidopsis thaliana
CDNA clone 006-G10, mRNA sequence.
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Paz-Ares,J., Valencia,A., Costantino,P., Vittorioso,P., Davies,B.,
Gilmartin,P., Giraudat,J., Parcy,F., Reindl,A., Sablowski,R.,
Coupland,G., Martin,C., Angenent,G.C., Baeumlein,H., Mock,H.P.,
     Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons, rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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                                                                                                                                                                               CTGTTGGAGGAGGCTTTAGGAGGAACAAGAAGCAAATCCAGATCGAAATCTACGGTCG
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Lechanty add-lugh-lugual.117.

Definition of the terms used to describe the quality of the clone: The about 2250 sequences from the clone collection were sorted according to clones and clustered. If more than one contig was formed, the clone was designated 'Contamination'. The contigs and singletons were blasted against CDS plus pseudogenes from the TIGRV5 annotation, and the resulting ACI code is presented if more than 90 percent identity was found. The sequences were also blasted against all TIGRV5 introns, and matches longer than 50 by with 95 percent identity are reported as 'intron found'. The remaining terms for Sequalaylysis describe the outcome of the evaluation of the CDS detected after pairwise alignment with CDS plus pseudogenes from the TIGRV5 annotation file. The sequences or contigs for which a full CDS with or without STOP codon was detected, a BLASTP against all TIGRV5 protein sequences was detected, a BLASTP against all TIGRV5 full good: better than 95 percent identity over more than 95 percent of the sequence; partial good: better than 95 percent of the sequence; martial good: better than 95 percent of the sequence; martial good: better than 95 percent of the sequence; no similarity; no hit from BLASTP. Note that the collection contains a few clones for which sequencing was not successful, which could have simple technical reasons.

Obviously, information about these clones is missing in the front transfer transfer transfer transfer. William State of Experiments and the second of the second /....= voci DH5alpha"
/lab host="E. coli DH5alpha"
/clone_lib="WPIZ-ADIS-065d"
/clone_lib="WPIZ-ADIS-065d"
/note="Vector: pDONR201; In the context of the EU-funded project REGIA (GLG-CT11999-00876, coordinator Javier Paz-Ares), a set of transcription factor ORFs was generated. The ORFs were produced in a decentralized way in the labs of the participants. Most of the ORFs were generated by RT-PCR using cDNA from various A. thaliana tissues as template. Initially, it was planned to use yeast recombination to move the ORFs from the cloning vectors into target constructs. For this reason, a number of the clones contain 'REGIA tags' (RG_tag1:
5pr-AATTCCAGCCACC-3pr; RG tag2:
5pr-CATGGCAATTCCCGGGGATC-3pr). During the lifetime of the Paz-Ares, Costantino, Vittorioso, Davies, Gilmartin, Giraudat, Parcy, Sabl owski, Coupland, Martin, Angenent, Baeumlein, Carbonero, Colombo, Tonelli, Engstroem, Droege-Laser, Gatz, Kavanagh, Kushnir, Zabeau, Laux, Holdsworth

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project, the GATEWAY system became available and finally all ORFs were transferred into GATEWAY vectors. At the end of the REGIA project, the clones were collected as plasmid DNA. For end-sequencing at the DNA core facility of the MPI of Plant Breeding Research (ADIS, head: Bernd Weisshaar), the plasmids were re-transformed into DHSalpha, arrayed into 96-well plates and new plasmid DNA was prepared. Re-transformation proved to be difficult because a number of clones displayed poor growth. Data submission has been handled by GabiPD (http://gabi.rzpd.de)."
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                                                                                                                                                                                                                       8.9%; Score 671.4; DB 8; Length 866;
larity 88.1%; Pred. No. 4.8e-109;
Conservative 0; Mismatches 12; Indels 93;
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Citrus clementina

Citrus clementina

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosids; eurosids II; Sapindales; Rutaceae; Citrus.

I (basea 1.0, 733)

Rorment, J., Gadea, J., Huerta, L., Abizanda, L., Agusti, J., Alamar, S., Alos, E., Andres, F., Arribas, R., Beltran, J.P., Berbel, A.,

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Terol, J., Trenor, M., Vaello, L., Vicente, O., Vidal, Ch., Zacarias, L.,

Descolations of the control of a citrue grannearia of European and Connearias.
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                                                                                                                                                                        CX308688 133 bp mRNA linear EST 06-MAY-2005 C21002G02Rv AbgLeaSubl Citrus clementina cDNA clone C21002G02, mRNA
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Genomics Laboratory
Instituto de Biologia Molecular y Celular de Plantas (Universidad
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/lab_host="Escherichia coli"
/lab_host="AbsLeaSub1"
/loto="Organ: laaves; Vector: pCR2.1; Subtracted cD1
library made from laminar abscision zone of leaves"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Development of a citrus genome-wide RST collection and cDNA microarray as resources for genomic studies Plant Mol. Biol. 57 (3), 375-391 (2005)
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Location/Qualifiers
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5073 GGACCGGTTTCACCTCCAACAACTCAACAGGCCATCTCTCATTCTA
765 GGAACGGTTTCACCTCCAACAACACACAGGCCATCTCTCATTCAA
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/organism="Citrus clementina"
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/cultivar="Clemenules"
/db_xref="taxon:85681"
/clone="C21002G02"
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Salanoubat, M., Choisne, N., Artiguenave, F., Brottier, P., Wincker, P., Samson, D., Saurin, W., Weissenbach, J. and Quetier, F.
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Submitted (25-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRX cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr |
Location/Qualifiers
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/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

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/db xref="taxon:3702"

/clone="F9G12"

/clone="F9G12"

/clone="lab="IGF"

/cotype="Columbia"
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1 (bases 1 to 597)
Walbot, V.
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1119111D07.y1 1119 - RescueMu Grid AA Zea mays genomic, genomic
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/culTivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
                  Indels
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Stanford University
855 California Ave, Palo Alto, CA 94304, USA
121 650 723 2227
Fax: 650 725 8221
                   ;
0
Pred. No. 1.6e-83;
; Mismatches 0;
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/organism="Zea mays"
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plate: 1119111 row: 2
Class: transposon-tagged.
Location/Qualifiers
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CG729372
CG729372.1 GI:37771010
                                                    2007 TTTATTTTGTTAAAGGCATTT
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and

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Venically, v.C.

Arabidopsis Genomic Sequence Database To Identify Minimal Overlaps for Arabidopsis Genomic Sequencing
Unpublished (1997)
Unpublished (1997)
Contact: Steve Rounsley
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Fax: 301 838 0208
Seq primer: M13-21
Class: BAC ends
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/clone lib="IGF"
/note="Vector: BelobBCII; Site_1: EcoRI; Site_2: EcoRI;
Produced by Thomas Altmann"
                 rosids, eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 486)
Rounsley, S.D., Kelley, J.M., Field, C.E., Craven, M.B., Adams, M.D. Venter, J.C.
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Best Local Similarity 98.1%; Pred. No. 1.3e-71;
Matches 477; Conservative 0; Mismatches 8;
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Location/Qualifiers
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/clone="F9G12"
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                            /clone lib="mill - RescueMu Grid AA"
/clone lib="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site l: BamHi, Site_2: BgJII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu.' Grid AA was grown at UC San Diego in 2002. DNA was extracted from leaf strips, double digested using BamHI and BgIII, and ligated to form circular plasmids. DHIOB calls were transformed and then screened on LB plates with ampicillin."
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F9G12TF IGF Arabidopsis thaliana genomic clone F9G12, genomic
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
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                                                                                                                                                                                                                                                                                                             Query Match 6.3%; Score 477.4; DB 10; Length Best Local Similarity 90.8%; Pred. No. 1.6e-74; Matches 524; Conservative 0; Mismatches 41; Indels
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                 /lab_host="DH10B"
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Gaps

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פפו-MAR-1998 בשימו באמן 433 bp DNA linear GSS 31-MAR-1998
F18P18TFB IGF Arabidopsis thallana genomic clone F18P18, genomic
Burrey sequence.
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363 CTTGCCTCCTCCAAAGCCTTGGAGATTACAATTCAAGCAACACTGGATTAGATTTGG 422
                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 433)
Rounsley, S.D., Field, C.E., Bass, S., Linher, K., Linher, K., Granger, D., Suh, E., Wible, C., Adams, M.D. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sex="hermaphrodite"
/clone llb="IGF"
/note="Vector: BeloBACII; Site_1: BCORI; Site_2: ECORI;
Produced by Thomas Altmann"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A BAC End Sequence Database for Identifying Minimal Overlaps in Arabidopsis Genomic Sequencing. Update 3 Unpublished (1997)
Other_GSSs: F18P18TR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Steve Rounsley
Department of Bukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/mol_type="Columbia"
/db_xref="taxon:3702"
/clone="F18P18"
                                                                              452
                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
                                         4651 TGGAACTCAAATAAGCAACATGATAAGTGG
                                                                              423 regaacrcararacecaacarearaceree
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Location/Qualifiers
1. .433
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Seq primer: M13-21
Class: BAC ends
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Matches 432; Conservative
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                                                                                                                                                                                                Spermatophyta; Magnoliophyta; audicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 452)

1 (bases 1 to 452)

1 (bases 1 to 452)

2 Rounsley, S.D., Suh, B.J., Wible, C., Golden, K., Shatsman, S., Choi, P., Yu, K., Akinretoye, B., Shen, K., Goonasekaram, S., Militscher, J., Adams, M.D. and Venter, J.C.

A BAC End Sequence Database for Identifying Minimal Overlaps in Arabidopsis Genomic Sequencing. Update 4

Unpublished (1998)

Other GSSs: P24E16TR

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Email: rounsley@tigr.org
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                        AQ011657 452 bp DNA linear GSS 29-MAY-1998 F24E16TFB IGF Arabidopsis thaliana genomic clone F24E16, genomic
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Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
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/note="Vector: BeloBACII; Site_1: EcoRI; Site_2: EcoRI;
Produced by Thomas Altmann"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  183 TCCTGTTGGAGGAGGCTTTAGGAGGAACAAGAAAACCAGAATCGAAATCTACGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 303 AAACCCTAGCAAGTCTCATAGCTACGGTCAAATCCCGGAGTTTAATTCCAACTTGCCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 TAGATGIGACTCAACCAATACTAAGTTCTGTTACTTCAATAACTATAGCCTTACTCAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4231 AATGGTGGAACGTGCTCGGATCGCAAAAGTCCCATTGCCTGAAGCAGCTCTAAATTGCCC
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/ecotype="Columbia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: rounsley@tigr.org
Seg primer: M13-21
Class: BAC ends
High quality sequence stop: 452.
Location/Qualifiers
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/clone="F24E16"
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                                                          survey sequence.
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Search completed: December 31, 2005, 05:09:55 Job time : 17838 secs
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/note="PCR was performed on DNA for primary transformants of Orysa sativa plants. The DNA forgment(s) resulting of PCR were directly sequenced from the left border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display is available from june 2004 at http://genoplante-info.infobiogen.fr/oryzatagline/. This sequence has been generated in the framework of the French plant genomics program Genoplante framework of the framework of the framework of the french former fo
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Sukaryota, viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Enthartoideae; Oryzae; Negad, P., Bourgeois, E., Meynard, D., Perin, C., Bourgeois, E., Meynard, D., Perin, C., High throughput T-DNA insertion mutagenesis in rice: A first step towards in silico reverse genetics
Contact: Guiderdoni
UMR PIA Biotrop program
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLS17384 1shing Sequence Tag of Oryza sativa T-DNA insertion lines Oryza sativa (japonica cultivar-group) genomic, genomic survey
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| mol type="genomic DNA"
| cultivar="Nipponbare"
| db_xref="taxon:39947"
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http://genoplante-info.infobiogen.fr)."
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Class: TDNA tagged.
    Location/Qualifiers
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TTGTAGAAGCCATCTTCCTTTCTACTGTCCTTTCGATGAAGTGACAGATAGCTGGCCAA
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AL132975.1 GI:6434228
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosida; eurosida II; Brassicales; Brassicaceae; Arabidopsis.
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    103240
    organism="Arabidopsis thaliana"
| formol_type="genomic DNA"
    db_xref="taxon:3702"
    /chromosome="3"

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/gene="T22E16.10"
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
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Minimum DB Maximum DB

Database

Result No.

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15214. .15369)
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/note="Contains Ubiquitin-conjugating enzymes active site
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note="EMBL:AF155818 most likely is not full length,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17259. .18094
/gene="T2En6.50"
join(17259. .17479,17564. .17699,17867. .18094)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="ubiquitin-conjugating enzyme UBC3"
/protein_id="CAB75896.1"
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                                      herfore N-terminal stretch"
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|gene="T22E16.40"
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/gene="T22E16.40"
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/gene="T22E16.30"
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'gene="T22E16.40"
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/gene="T22E16.40"
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                                                                                                                                                                                                                                                                                                                                                                              VGDSGFPLLPWLLTPYGKPTSLPOTEFNKRHSEATKAQMALSKLKDRWRIINGVWW
MPDRNRLPRIIFVCCLLHNIIIDMEDQTLDDQPLSQQHDMNYRQRSCKLADEASSVLR
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spliced variant, Homo sapiens, EMBL:AF038958"
                                      note="similarity to predicted proteins, Arabidopsis
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complement (3660. .3728)
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/db_xref="G1:7076782"
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            GCATCTTGAACGATAGCCTTTCCTTTATCGCAATGATGGCATTTGTAGAAGCCATCTTCC
                            TTTTCTACTGTCCTTTCCATGAAGTGACAGATAGCTGGGCAATGGAATCCCGAGGAGTTT
                                                                                                                                              CCCGATATTACCCTTTGTTGAAAGTCTCAATAGCCCTCTGGTCTTCTGAGACTGTATCT
                                                                                                                                                                      CCCGATATTACCCTTTGTTGAAAAGTCTCAATAGCCCTCTGGTCTTCTGAGACTGTATCT
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                                                                              TTTTCTACTGTCCTTTCGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGGTTT
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GSTLYTHILKSLEAGOGFKSVVANIGLPNDPSVRMHEALGYAPRGMLRAAGFKHOWHD
VGFWQLDFSLPVPPRPVLPVTEM"
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                          Activation-tagging vector pSKI015
Activation-tagging vector pSKI015
other sequences; artificial sequences; vectors.

1 (bases 1 to 10138)
Weigel,D., Ahn,J.H., Blazquez,M.A., Borevitz,J.O.,
Christensen,S.K., Fankhauser,C., Ferrandiz,C., Kardailsky,I.,
Malancharuvil,E.J., Neff,M.M., Nguyen,J.T., Sato,S., Wang,Z.,
Xia,Y., Dixon,R.A., Harrison,M.J., Lamb,C.J., Yanofeky,M.F. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4261 TAGTITCGGATCTAGATATCACATCAATCCACTTGCTTTGAAGACGTGGTTGGAACGTCT
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                                                                                                                                                                                                                                                     Kardailsky, I. and Weigel, D.
Direct Submission
Submitted (IT-SEP-1999) Plant Biology Laboratory, The Salk
Institute for Biological Studies, 10010 N. Torrey Pines Road,
Jolla, CA 92037, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="promotes resistance to glutamine synthetase inhibitors"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18.5%; Score 1402.4; DB 11; Length 10138; ilarity 99.9%; Pred. No. 1.7e-195; Conservative 0; Mismatches 1; Indels 0; G
                                                                                                                                                                                                                                                                                                                                                            1. .10138
/organism="Activation-tagging vector pSKI015"
/mol_type="genomic DNA"
/db_xref="taxon:109189"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2894. .4178
/note="caulfilower mosaic virus 35S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2830, .2849
/note="T7_RNA polymerase promoter"
                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="T7 RNA polymerase promoter" 36. .2204
                                                                                                                                                                                 Activation tagging in Arabidopsis
Plant Physiol. 122 (4), 1003-1013 (2000)
10759496
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/product="mannopine synthase"
/note="5' end and promoter"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="dervied from pUC19"
2205. 2662
/note="derived from phage fl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7690. .7713
/note="T-DNA left border"
complement (8054. .8784)
/product="octopine synthase"
/note="3' end"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2663, .2829
/note="derived from pUC19"
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4270. 4294
/note="T-DNA right border"
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GI:6537289
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Best Local Similarity
Matches 1403; Conserv
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VERSION
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2663. .2205
/note="derived from phage fl"
2663. .2205
/note="derived from pUC19"
2830. .2849
/note="from T7 RNA polymerase"
2894. .4178
/note="from cauliflower mosaic virus 35S gene promoter"
4270. .4294
/note="r-DNA right border"
8054. .8784
/note="r-DNA left border"
8064. .8789
/note="includes mannopine synthase promoter and 5' UTR
7496
                                                                                                            3001 GATATTACCCTTTGTTGAAAAGTCTCAATAGCCCTCTGGTCTTCTGAGACTGTATCTTTG 2942
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Christensen, S.K., Fankhauser, C., Ferrandiz, C., Kardailsky, I.,
Malancharuvil, E.J., Neff, M.M., Nguyen, J.T., Sato, S., Wang, Z.,
Xia, Y., Dixon, R.A., Harrison, M.J., Lamb, C.J., Yanofsky, M.F. and
Chory, J.
                                                                                                                                                                                               2941 ATATTCTTGGAGTAGACGAGGTCGTGCTCCACCATGTTGGGGATCCACTAGTTCTAG
                                                                                     GATATTACCCTTTGTTGAAAAGTCTCAATAGCCCTCTGGTCTTCTGAGACTGTATCTTTG
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Pines Road,
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/organism="Activation tagging vector pSKI074"
/mol type="other DNA"
/bb xref="taxon:112458"
/note="from T7 RNA polymerase"
                                                                                                                                                                                                                                                                                                                                                                                                                  DNA circular (complete sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence"
8756. .9739
Product="neomycin phosphotransferase"
8771. .9565
/function="confers kanamycin resistance"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Activation tagging vector pSK1074
Activation tagging vector pSK1074
other sequences; artificial sequences; vectors.
(bases 1 to 10450)
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Plant Physiol. 122 (4), 1003-1013 (2000)
10759496
                                                                                                                                                                                                                                                                                                                                                                                                           Activation tagging vector pSKI074, AF218466.1 GI:6715465
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                                                                                                                                                                                                                                                                                     2881 AGCGGCCGCCACCGCGGTGGAGCT 2858
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCATCTTGAACGATAGCCTTTCCTTTATCGCAATGATGGCATTTGTAGAAGCCATCTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCCGATATTACCCTTTGTTGAAAAGTCTCAATAGCCCTCTGGTCTTCTGAGACTGTATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTGATATTCTTGGGAGTAGACGAGAGTGTCGTCCACCATGTTGGGGATCTAGATATCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3601 AGAGTGTCGTGCTCCACCATGTTGGGGATCTAGATATCACATCAATCCACTTGCTTTGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCCGATATTACCCTTTGTTGAAAGTCTCAATAGCCCTCTGGGTCTTCTGAGACTGTATCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATCAATCCACTTGCTTTGAAGACGTGGGTTGGAACGTCTTCTTTTTCCACGATGTTCCTC
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larity 99.9%; Pred. No. 1.7e-195;
Conservative 0; Mismatches 1; Indels 0; G
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An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al. (1998) Plant J. 15:707-720; Seki et al. (2002) Science 296:141-145.

This clone is in a modified pBluescript vector.

Please visit our web site (http://rarge.gsc.riken.jp/) for further
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             424 TCAACCTCGCCATTTCTGCAAAACATGTCGTCGTCGTTGGACACGTGGCGGTTCCTTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           664 GCCCATCTTGCCTCCTCTCCAAAGCCTTGGAGATTACAATTCAAGCAACACTGGATTAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAATTCAATGGTGGAACGTGCTCGGATCGCAAAAGTCCCATTGCCTGAAGCAGCTCTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     304 GAATTCAATGGTGGAACGTCCGATCGCAAAAGTCCCATTGCCTGAAGCTCTAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            244 CTIACGGCGGCTCTCATCACCACCACCGACTTCTCAGGTTGCAGGTTCAGGTCAAGGTTAGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4345 TCAACCTCGCCATTTCTGCAAAACATGTCGTCGCTATTGGACACGTGGCGGTTCCTTGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
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note="common name: thale cress"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="At3g55370"
134. .1105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene="At3g55370"
                                                                                                                                                                                                                                                                                                      chromosome="3"
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Best Local Similarity 93.2
Matches 1266; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           . .1457
                                                                                                                                         details.
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I otoki,Y., Seki,M., Ishida,J., Nakajima,M., Enju,A., Kamiya,A., Narusaka,M., Shin-i,T., Nakagawa,M., Sakaki,Y., Sakurai,T., Iida,K., Kohara,Y., Kobayashi,M., Toyoda,A., Sakaki,Y., Sakurai,T., Iida,K., Akiyama,K., Satou,M., Toyoda,T., Konagaya,A., Carninci,P., Kawai,O., Hayashizaki,Y. and Shinozaki,K.

I Submitted (12-MAR-2005) Motoaki Seki, RIKEN Genomic Sciences Center; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail:mseki@gsc.riken.jp, URL:http://rarge.gsc.riken.jp/, Tel:81-45-503-9625,
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Arabidopsis thaliana gene for zinc finger protein OBP3, complete cds, clone: RAFL25-48-C17.
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Kang,H.G. and Singh,K.B.
Direct Submission
Direct Submission
Submitted (ND-1999) MCDB, University of California, 1900 MCDB, 405 Hilgard Ave., Los Angeles, CA 90095, USA Location/Qualifiers
1. 1274
/organism="Arabidopsis thaliana"
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138. -932 /note="transcriptional activator"

ecotype="Columbia"

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                                      Gaps
   15; Length 1274;
                                      93;
                                      3; Indels
Score 1156.2; DB 15
Pred. No. 2.9e-159;
0; Mismatches 3;
 Query Match 15.3%;
Best Local Similarity 92.9%;
Matches 1261; Conservative
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PLN 23-DEC-1999 complete cds.

AF155818 1274 bp mRNA linear Arabidopsis thaliana zinc finger protein OBP3 mRNA, AF155818

AF155818.1 GI:5059397

DEFINITION ACCESSION VERSION KEYWORDS

RESULT 5 AF155818 LOCUS

SOURCE ORGANISM

REFERENCE AUTHORS TITLE

JOURNAL

Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Brakaryota; Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Wagnollophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

Kang, H.G. and Singh, K.B. Characterization of Arabidopsis Dof Transcription Factors, a Novel Zinc Finger Protein Family in Plants Unpublished

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9105 GAIGGCATTIGIAGAAGCCATCTTTCTACTGTCCTTTCGAIGAGGAGAGAGATAG
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                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                               DB 11; Length 9663;
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  /mol_type="other DNA"
/db_xref="taxon:188057"
/note="Tobacco rattle virus RNA2-based T-DNA
synonym: pYL156"
1. 1639
/note="TWY strain ppk20 RNA2 5'-sequence"
1640. :1708
/note="TRV strain ppk20 RNA2 3'-sequence"
1709. :2103
/note="TRV strain ppk20 RNA2 3'-sequence"
2104. :2154
/note="synthetic sequence"
2155. :8894
/note="pyanbia 0390 sequence"
8895. :9663
                                  T-DNA
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                                                                                                                                                                                              1895. .9663
note="CaMV 35S promoter from pCASS2"
                                                                                                                                                                                                                                               8.4%; Score 640.2; DB 11;
98.4%; Pred. No. 3.9e-84;
rative 0; Mismatches 3;
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Best Local Similarity 98.4
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Formence:
AF406991 GI:21389151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            1945 AGAGAATGATCAGGATCGGGGTAGGGATGGGGATGGAGTGAATAACTTATCAAGAAACTT
                                                                                                                                                                                              TTTGGGTAATATCAACATAAACTCAGGCAGGAAGGAATACACACATCATGGGGAGGTAA
                                                                                                                                                                                                           938 CAGCACTAGCTATTCTTGATGATTCTTTTTTTTGTTGGGGGGTGTACATTGGTGCTTGTCCAT
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                                       TAATCAAGGTGATTCTCAACAGAAGAGTGATTATTTCCAATCAGCTAATGTTTAAGCC
                                                                                          1885 CITGAIGGAITITITCITCAGGCGGGTIAGCGCCACGCAAACAAGAAAIGIGAAGGCGGA
                                                                                                          158 AGAGAATGATCAGGATCGGGGTAGGGATGGGGATGGAGTGAATAACTTATCAAGAAACTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tobacco rattle virus RNA2-based VIGS vector pTRV2 (pYL156) Tobacco rattle virus RNA2-based VIGS vector pTRV2 other sequences; artificial sequences; vectors.

Liu, Y., Schiff, Marathe, R. and Dinesh-Kumar, S.P.
Tobacco Rarl, EDS1 and NPR1/NIM1 like genes are required for N-mediated resistance to tobacco mosaic virus
Plant J. 30 (44), 415-429 (2002)
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CITITITEGEGETCATIGAATAATCATCGAATTCTC 5461
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Submitted (08-AUG-2001) MCDB,
New Haven, CT 06520, USA
Location/Qualifiers
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AIV3/283 12607 bp DNA circular SYN 02-MAR-2005
C-terminal TAP T-DNA vector pYL436, complete sequence.
AY37283
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Ja (bases 1 to 12607)

Liu, Y. and Dinesh-Kumar, S.P.

Direct Submission

Sibmitted (28-AUG-2004) MCDB, Yale University, New Haven, CT 06520, USA
                                                                                                                                                                                                6730 CTGGGCAATGGAATCCGAGGAGGTTTCCCGATATTACCCTTTGTTGAAAAGTCTCAATAG 6789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C-terminal TAP T-DNA vector pYL436
C-terminal TAP T-DNA vector pYL436
other sequences; artificial sequences; vectors.
I (bases 1 to 12607)
Rubio, V., Shen, Y., Saijo, Y., Liu, Y., Gusmaroli, G.,
Dinesh-Kumar, S.P. and Deng, X.W.
An alternative tandem affinity purification strategy applied to Arabidopsis protein complex isolation
Plant J. 41 (5), 767-778 (2005)
271 CATCTTTGGGACCACTGTCGGTAGAGGCATCTTGAACGATAGCCTTTCCTTTATCGCAAT
                                                                                                                                                 211 GATGGCATTTGTAGAAGCCATCTTCCTTTTCTACTGTCCTTTCGATGAAGTGACAGATAG
                                                                                                                                  6670 GATGGCATTTGTAGAAGCCATCTTCCTTTTCTACTGTCTTTCGATGAAGTGACAGATAG
                                                                 CATCTTTGGGACCACTGTCGGTAGAGGCATCTTGAACGATAGCCTTTTCCTTTATCGCAAT
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/organism="C-terminal TAP T-DNA vector pyL436"
/or_type="cther DNA"
/db_xref="taxon:293967"
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/note="attR1-CmR-ccdB-attR2 GATEWAY cassette"
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/note="duplicated CaMV 35S promoter"
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/note="protease 3C cleavage site"
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/note="2x IgG binding domain"
3670. 3932
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/note="TMV U1 omega sequence"
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1163. .3180
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Location/Qualifiers
1. .12337
/organism="N-terminal TAPA T-DNA vector pN-TAPa"
                                                                                           N-terminal TAPA T-DNA vector pN-TAPa
N-terminal TAPA T-DNA vector pN-TAPa
other sequences; artificial sequences; vectors.
1 (basea to 12537)
Rubio, V., Shen, Y., Saijo, Y., Liu, Y., Gusmaroli, G.,
Dinesh-Kumar, S.P. and Deng, X.W.
An alternative tandem affinity purification strategy applied to Arabioopsis protein complex isolation
Plant J. 41 (S), 767-778 (2005)
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/note="9x myc tag"
1704. .3577
/note="attR1-CmR-ccdB-attR2 GATEWAY cassette"
/note="nos terminator"
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/note="TMV Ul omega sequence"
854. .1231
/note="2x protein A IgG binding domain"
1256. .1279
/note="protease 3C cleavage site"
                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="other DNA"
/db_xref="taxon:300483"
/noce="derived from pPZP222"
/noce="duplicated CaMV 35S promoter"
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                 DNA
        N-terminal TAPA T-DNA vector pN-TAPA, AY788908.1 GI:55824365
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note="6x HIS tag"
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Rubio, V. and Deng, X.W.
Direct Submission
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CVUI0488 8626 bp DNA circular SYN 28-JAN-1995 Binary cloning vector pPZP121 for plant transformation, complete sequence.
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Cloning vector pPZP121
other sequences; artificial sequences; vectors.
I (bases 1 to 8626)
Hajdukiewicz, P., Svab, Z. and Maliga, P.
The small, versatile pPZP family of Agrobacterium binary vectors
For plant transformation
Plant Mol. Biol. 25 (6), 989-994 (1994)
2 (bases 1 to 8626)
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1043 IGCICCICGIGGGGGGGGGCCCAICTIGGGACCACTGICGGAGAGAGAGAGACAICTIGAACGA
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                Score 621; DB 6,
Pred. No. 3e-81;
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                                            Gaps
                      DB 11; Length 12607;
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Unclassified.
Unclassified.
S McMullen,W.D., Roth,B.A. and Townsend,R.
Maize chlorotic dwarf virus and resistance thereto
Maize chlorotic dwarf virus and resistance thereto
Asize chlorotic dwarf virus and resistance thereto
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Pred. No. 3.6e-84;
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Sequence 1 from patent US 5569828.
128266
128266.1 GI:1819042
                     Best Local Similarity 98.4%;
Matches 660; Conservative
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Binary cloning vector pPZP221 for plant transformation, complete
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Direct Submission

Direct Submission

Submitted (09-JUN-1994) Peter Hajdukiewicz, Waksman Institute,
Submitted (09-JUN-1994) Old Hoes Lane, Piscataway, NJ 08855, USA

Location/Qualifiers
                                                                                                                                       Gaps
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                                                                                                                Score 617.2; DB 1.
Pred. No. 9.2e-81;
0; Mismatches 33
                                                             /organism="Cloning vector
/mol_type="genomic DNA"
/db xref="taxon:35364"
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Cloning vector pPZP221
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Best Local Similarity 93.6%;
Matches 659; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                2 (bases 1 to 8731)
Hajdukiewicz, P.
Hajdukiewicz, P.
Direct Submission
Submitted (09-JUN-1994) Peter Hajdukiewicz, Waksman Institute,
Rutgers University, Old Hoes Lane, Piscataway, NJ 08855, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
Cloning vector pPZP221
other sequences; artificial sequences; vectors.
1 (bases 1 to 8731)
Hajdukievicz, P., Svab, Z. and Maliga, P.
The small, versatile pPZP family of Agrobacterium binary
for plant transformation plant plant Mol. Biol. 25 (6), 989-994 (1994)
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/organisma="Cloning vector pPZP221"
/mol_type="genomic DNA"
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llarity 93.6%; Pred. No. 9.1e-81;
Conservative 0; Mismatches 33.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12;
complement(7334. .8114)
/note="CaMV35S2; CaMV 35S promoter, duplicated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 8742;
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Pred. No. 9.1e-81;
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                                                                              'note="Placz; lacz promoter"
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Matches 659; Conservative
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LOCUS
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Roberts, C., Rajagopal, S., Smith, L.M., Nguyen, T.A., Yang, W.,
Rugochu, S., Ravi, K.S., Vijayachandra, K., Harcourt, R.L.,
Dransfield, L., Desamero, N., Slamet, I., Hadjukiewicz, P., Svab, Z.,
Maliga, P., Mayer, J.E., Keese, P. K., Kilian, A. and Jefferson, R.A.
A comprehensive set of modular vectors for advanced manipulations
and efficient transformation of plants
L. Unpublished
L. Full description of constructs
S. Woberts, C., Rajagopal, S., Smith, L.M., Nguyen, T.A., Yang, W.,
Nugrobu, S., Ravi, K.S., Vijayachandra, K., Harcourt, E.,
Dransfield, L., Desamero, N., Slamet, I., Hadjukiewicz, P., Svab, Z.,
Maliga, P., Mayer, J.E., Keese, P.K., Kilian, A. and Jefferson, R.A.
Direct Submission
L. Submitted (15-FEB-2000) CAMBIA, Clunies Ross St., Black Mountain /
GPO Box 3200, Canberra, ACT 2601, Australia
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MAKORISPELKKLIEKYRCVKDTEGMSPAKVYKLVGENENLYLK
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EDTPPROPRELYDFLKTEKPERELYFSHGDLGDSNIFVKDGKVSGFIDLGRSGRADKW
                                                       circular SYN 24-APR-2000
                                                                                                                                                                                                                 other sequences; artificial sequences; vectors.

(sites)
Hajdukiewicz, D., Svab, Z. and Maliga, P.
The small, versatile pP2P family of Agrobacterium binary vectors for plant transformation
Plant Mol. Biol. 25 (6), 989-994 (1994)
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/note="pBR322 origin of replication"
complement(4954. .5748)
/note="aadA (kanamycin resistance) gene amplified from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YDIAFCVRSIREDIGEEQYVELFFDLLGIKPDWEKIKYYILLDELF"
6173. .6198
//note="left border repeat from C58 T-DNA"
6265. .65. .65. .7004
//note="camv 3'UTR (polyA signal)"
complement(6506. .7303)
//note="nptil (kanamycin resistance) gene"
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/product="aminoglycoside phosphotransferase"
/protein id="Aminoglycoside phosphotransferase"
/db_xref="G1:7638147"
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                                                                                   complete sequence
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/db_xref="G1:7638148"
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Binary vector pCAMBIA-2300,
AF234315
AF234315.1 GI:7638145
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Binary vector pCAMBIA-2300
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VERSION
KEYWORDS
SOURCE
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TITLE
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AUTHORS
        RESULT 12
AF234315
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Solves, 8909 bp DNA circular SYN 28-JAN-1995 Binary cloning vector pPZP111 for plant transformation, complete sequence.
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                                      /codon_start=1
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/db_xref="G1:7638139"
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                                                                                                                                                                                                                                                                                                  DB 11; Length 8894;
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/note="pUC18 MCS; polylinker"
8808. .8833
/note="right border T-DNA repeat"
                                                                                                                                                                                                                                                                                               Score 617.2; DB 1:
Pred. No. 9.1e-81;
'note="Placz; lacz promoter'
                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                  8.1%;
                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 93.6
Matches 659; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="chloramphenicol acetyl transferase"
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ANMDNFFAPVFTMGKYYTQGDKVLMPLAIQVHHAVCDGFFHVGRMLNBLQQYCDEWQGG
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                                                                                                                    1 (sites)
Hajdukiewicz,P., Svab,Z. and Maliga,P.
Hajdukiewicz,P., Svab,Z. and Maliga,P.
The small, versatile pPZP family of Agrobacterium binary vectors for plant transformation
Plant Mol. Biol. 25 (6), 989-994 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Full description of constructs
(bases 1 to 8894)

Roberts,C., Rajagopal,S., Smith,L.M., Nguyen,T.A., Yang,W.,
Nugrobu,S., Ravi,K.S., Vijayachandra,K., Harcourt,R.L.,
Dransfield,L., Desamero,N., Slamet,I., Hadjukiewicz,P., Svab,Z.,
Maliga,P., Mayer,J.E., Keese,P.K., Killan,A. and Jefferson,R.A.
Submisted (15-FEB-2000) CAMBIA, Clunies Ross St, Black Mountain /
GPO Box 3200, Canberra, ACT 2601, Australia
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/note="left border repeat from C58 T-DNA"
6417. .6620
/note="Camy 3'UTR (polyA signal)"
/note="aadA (kanamycin resistance) gene amplified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Binary vector pCAMBIA-2200"
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complement (980. .1980)
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complement (2573. .3573)
/note="STA region from pV81 plasmid"
complement (2573. .3573)
/note="bom site from pBR322"
complement (4383. .4443)
/note="bom site from pBR322"
complement (4383. .4663)
/note="cat (chloramphenicol resistance) gene from //note="cat (chloramphenicol resistance)
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protein_id="AAR65391.1"
db_xref="G1:7638137"
                                                                                   Binary vector pCAMBIA-2200
Binary vector pCAMBIA-2200
other sequences; artificial sequences; vectors.
  complete sequence
  Binary vector pCAMBIA-2200,
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Mydsrykgtyydverekommlwlegklpvpkvlhferhdgmsnllmseadgylcseey
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Edyfpkdprelydelkyerelbeelvfshgdlgdsnifvkoksgfidlgrsgradkw
Ydlafvchrsiredigeegyvelffdlgikdpwekikyyilldelf"
6557.,6582
                                                                                                        circular SYN 24-APR-2000
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Roberts, C., Rajagopal, S., Smith, L.M., Nguyen, T.A., Yang, W.,
Nugrobu, S., Ravi, K.S., Vijayachandra, K., Harcourt, R.L.,
Dransfield, L., Desamero, N., Slamet, I., Hadjukiewicz, P., Svab, Z.,
Maliga, P., Mayer, J.E., Keese, P.K., Kilian, A. and Jefferson, R.A.
A comprehensive set of modular vectors for advanced manipulations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Black Mountain /
                                                                                                                                                                                                                                          1 (sites)
Hajdukiewicz, P., Svab, Z. and Maliga, P.
The small, versatile pPZP family of Agrobacterium binary vectors plant transformation
Plant Mol. Biol. 25 (6), 989-994 (1994)
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(Loses 1 to 8958)

Roberts, C., Rajaopal, S., Smith, L.M., Nguyen, T.A., Yang, W.,

Roberts, C., Rajaopal, S., Smith, L.M., Harcourt, R. L.,

Nugrohu, S., Ravi, K. S., Vijayachandra, K., Harcourt, R. L.,

Dransfield, L., Desamero, N., Slamet, I., Hadjukiewicz, P., Svab, Z.,

Dransfield, L., Desamero, N., Slamet, I., Hadjukiewicz, P., Svab, Z.,

Dransfield, L., Desamero, N., Slamet, I., Hadjukiewicz, P., Svab, Z.,

Dransfield, L., Desamero, N., Slamet, I., Hadjukiewicz, P., Svab, Z.,

Direct Submission

Submitted (15-FEB-2000) CAMBIA, Clunies Ross St, Black Mountain /

GPO Box 3200, Camberra, ACT 2601, Australia

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene amplified from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (1364. .2364)
/note="STA region from pVS1 plasmid"
complement (2557. .3957)
/note="pVS1-REP; replication origin from pVS1"
complement (4367. .4627)
/note="bom site from pBR322"
/note="bom site from pBR322"
/note="bR322 origin of replication"
complement (5338. .6132)
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/protein_id="AAR65338.1"
/db_xref="GI:7638067"
8243 CCACCATGTTGGCAAGCTGCTCTAGCCAATACGCAAACCGCCTC 8286
                                                                                                                                                                                                                          Binary vector pCAMBIA-1300
Binary vector pCAMBIA-1300
other sequences; artificial sequences; vectors
                                                                                                                                  vector pCAMBIA-1300, complete sequence.
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/note="pUC18 MCS; polylinker"
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                                                                                other sequence; artificial sequences; vectors.

1 (bases 1 to 8909)
Hajdukiewicz,P., Svab,Z. and Maliga,P.
Hajdukiewicz,P., Svab,Z. and Maliga,P.
for small, versatile pPZP family of Agrobacterium binary vectors for plant transformation
Plant Mol. Biol. 25 (6), 989-994 (1994)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7835 TTTGTTGAAAAGTCTCAATAGCCCTTTGGTCTTCTGAGACTGTATCTTTGATATTCTTGG
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                                                                                                                                                                                                                                                    2 (bases 1 to 8909)
Hajdukiewicz, P.
Direct Submission
Submitted (09-UUN-1994) Peter Hajdukiewicz, Waksman Institute,
Rutgers University, Old Hoes Lane, Piscataway, NJ 08855, USA
1. 6909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 11; Length 8909;
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                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Cloning vector pPZP111"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 617.2; DB 1:
Pred. No. 9.1e-81;
0; Mismatches 33,
                                             Cloning vector pPZP111
Cloning vector pPZP111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 8.1%;
Best Local Similarity 93.6%;
Matches 659; Conservative 0
    GI:506682
    010487.1
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                                               SOURCE
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Combreanton (1) (1) (hygromycin resistance) gene"

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/note="left border repeat from C58 T-DNA"
6649. .6857
/note="CaMV 3'UTR (polyA signal)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (7934. .8714)
/note="CaMV358; 358 promoter from CaMV"
8862. .8916
/note="Placz; lacz promoter"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 617.2; DB 1
Pred. No. 9.1e-81;
0; Mismatches 33
                                                                                                                      complement (6873. .7898
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Best Local Similarity 93.6
Matches 659; Conservative
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Post-processing: Listing first 45 summaries

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SUMMARIES

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New transgenic plant cell, useful in producing plants with altered size and stature and with normal and healthy root growth.

WPI; 2004-225757/21. P-PSDB; ADL71830.

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Claim 24; SEQ ID NO 1; 53pp; English.

Aaa56878 Constitu Aaa51890 Chimaeri Adb64406 CaMV 35 Aan80891 Sequence Abv75872 Vector E Aaa17547 Plasmid Aaa47492 pB2LRA p Aaa47492 pB1LRA p Aaa47499 pB1LRA p	AA247494 AA247495 AA247495 AA17548 AAC53317 AAC83317 AAC88405 AAC89826 AAC89826 AAC89826 AAC89826 AAC89826	ALIGNMENTS . tion factor; ocs binding factor; growth; plant; gene; ds; OBF;	sis thalian
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The invention relates to a transgenic plant transformed by a Dof transcription factor, OBF (ocs binding factor) binding protein (OBF3). OBF3 is also known as SOB1. The transgenic plant cell and OBF3 nucleic acid and polypeptides are useful in producing transgenic plants with altered size and stature and with normal and healthy root growth. The present sequence is Arabidopsis thaliana OBF3 DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTCGTGAAAAAATGCGCATGTTCTTGTTGGAATCTAGGAATCTTCTTCTACTAAAGATG
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which is responsible for many red and blue colours in plants. The polynucleotide is useful for modifying e.g. leaf colour, flower colour fruit colour in plants. The present sequence represents the plasmid pAG3202 which is used in an example from the present invention for the generation of plants with an ANTI phenotype by transformation with an activation tagging construct
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Oy 7259 TTCCACGATGTTCCTCGTGGGGGGTCCATCTTTGGGACCACTGTCGGTAGAGGCATC 7318 Db 17899 TTCCACGATGTTCCTCGTGGGTGGGGGGTCCATCTTTGGGACCACTGTCGGTAGAGGCATC 7319 TTGAACGATGTTCCTTTATCGCATGATGTTTGTAGAAGCCATCTTCCTTTTC 7378 17839 TTGAACGATAGCCTTTCCTTTATCGCAATGATGGCATTTGTAGAAGCCATCTTCCTTTTC 7378 17839 TTGAACGATAGCCTTTCCTTTATCGCAATGATGGCATTTGTAGAAGCCATCTTCCTTTTC 7378 17739 TACTGTCCTTTCGATGAAGTGACAGATAGCTGGAATGCAATGAAGCCATCTTCCTTTTC 17780 Oy 7379 TACTGTCCTTTGAAAAGTGTCAATAGCTGGACATCTAGAATCCCAAGAAGTTTCCCGA 17720 Oy 7439 TATTACCCTTTGTTGAAAAGTCTCAATAGCCTCTTGTGAAATCCCAAGAACTTTCCTTTGA 17720 Oy 74499 TTCTTGGAAGAAAAGTCTCAATAGCCCTCTGGTCTTCTTGAAATTTGTAGAACTTTTGAT 17600 Oy ATTCTTGGAAGAAAAGTCTCAATAGCCCTCTGGTCTTTTTGAT 17600 Oy ATTCTTGGAAGAAGTGTCAATAGCCCTCTGGTCTTTTTTTT	RESULT 6 AAA88401/C ID AAA88401 standard; DNA; 1361 BP. XX AC AAA88401;	09-JAN-2001 4X CaMV 35S CaMV; 35S;	activation tagging; fruit; transgenic Cauliflower mosaic virus. Key Location/Qualifiers repeat_region 11354	repeat_unit	/+tag= c //htag= c //nte= "CaMV 35S enhancer AluI-EcoRV fragmen enhancer 130. 331 //ntag= d //note= "129 bp fragment of the CaMV sequence enhancer //tag= e	repeat_unit = 3 enhancer = 3 enhancer	nit 66/	
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is that of a 4X cauliflower mosaic virus (CaMV) 35S chancer sequence preferred for use in the method of the invention. It includes 4 repeats of 202 bp Alui-EcokV fragments of the 35S enhancer, 2129 bp of the CaMV sequence associated with each tandem Alu-EcokV repeat, 2129 bp of the CaMV sequence associated with each tandem Alu-EcokV repeat, 2129 bp of the CaMV sequence, which does not appear in the cand an additional 7 bp repeated sequence, which does not appear in the companient of the native CaMV genome. This 4K CaMV 35S enhancer element can be used in a method for identifying genes associated with a desired trait in a fruit-bearing plant. The method involves: transforming CC plant cells with an activation tagging vector comprising an element which functions to enhance gene expression and has the ability to integrate into the plant genome in a manner effective to enhance expression of canive plant genes, selecting plant cells. regenerating cransformed plant cells to yield mature plants, selecting plants having a casived trait, identifying, isolating and characterizing genes the contribution of which has been enhanced, and confirming the contribution of the modified seed number, plants pathogens, insects, modified seed number, pattern or distribution of leaves and flowers modified seed number, pattern or distribution of leaves and flowers, modified seem length between nodes, root mass or root cand shape, modified seem length between nodes, root mass or root calculation and shape, and increased drought, salt and antibiotic contransers. Plants having short life cycles are transformed, as complified by dwarf varieties of tomato
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                                                       not associated with 35S enhancer"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Identifying genes associated with a desired trait for isolating and characterizing the genes comprises using an enhancer element which enhances gene expression and stably integrates into the plant genome.
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/note= "CaMV 35S enhancer AluI-EcoRV fragment"
1220. .1348
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        bp fragment of the CaMV sequence"
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"CaMV 35S enhancer unit 4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a transgenic plant transformed by a Dof transcription factor, OBF (ocs binding factor) binding protein (OBF3). OBF3 is also known as SOB1. The transgenic plant cell and OBF3 nucleic acid and polypeptides are useful in producing transgenic plants with altered size and stature and with normal and healthy root growth. The present sequence is Arabidopsis thaliana OBF3 antisense DNA.
TTGAACGATAGCCTTTCCTTTATCGCAATGATGGCATTTGTAGAAGCCATCTTCCTTTTC
                                                                                              TATTACCCTTTGTTGAAAAGTCTCAATAGCCCTCTGGTCTTCTGAGACTGTATCTTTGAT
                                                 TACTGTCCTTTCGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGGTTTCCCGA
                                                                                                                  TATTACCCTITGTTGAAAAGTCTCAATAGCCCTCTGGTCTTCTGAGACTGTATCTTTGAT
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                                                                                                                                                                                                                                                                                                                                                                                                             Transgenic plant; Dof transcription factor; ocs binding factor; plant size; plant stature; root growth; plant; gene; ds; OBF; OBF binding protein; OBP3; SOB1; mouse-ear cress.
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CATTATGAGACATTGAGACATCTATAGAACATATATGTAATGTATATAAACGTACTTAA
           GTCGAATTTTATGACCAAAGTAAATAAATTATGCCGAATGTACATGCTAATATGCGGTTT
                                                                                             TCACAATCATAATGGCCAACTAACTAATTGAAAAGACAATGGAATGACATGGA
                                         GTCGAATTTTATGACCAAAGTAAATAAATTATGCCGAATGTACATGCTAATATCGAGTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GITGGAAACITITITGTGTGTTCAITGAATAATCATCGAAITCTCAATITCTTGGAGACC
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                                                                                                                   Transgenic plant; Dof transcription factor; ocs binding factor; plant size; plant stature; root growth; plant; gene; ds; OBF; OBF binding protein; OBF3; SOB1; mouse-ear cress.
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Best Local Similarity 100.0%; Pred. No. 7e-308;
Matches 1062; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1062 BP; 348 A; 159 C; 155 G; 400 T; 0 U; 0 Other;
                                                                                                 Arabidopsis thaliana OBP3 antisense DNA #9
                                                                                                                                                                                                                                                                                                                                                                         Claim 40; SEQ ID NO 20; 53pp; English.
                                     ADL71848 standard; DNA; 1062 BP
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                                                                         TGAAAAACTATAATTAATCTGCAATTCTTGTCAAAGTAGTCACAATTTTTATCTATTTTC
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11.7%; Score 888; DB 12; L
Best Local Similarity 100.0%; Pred. No. 6.8e-256;
Matches 888; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                    121 ACAAAAAGAAATAAAGAGCCTAAGAGAATGATGAAAATTGAAAAGAGAAAAAGAGCATTG
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                                                                                                                                                    Claim 39; SEQ ID NO 19; 53pp; English
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                                                                                                                                                                                                                                    cell, useful in producing plants with altered size normal and healthy root growth.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 AGTACTTCATCACTTACTTCTCGCCCAAGTTACTCAAACCCTAGCAAGTTTCATAGCTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4496 AGTACTTCATCACTTACTTCTCGCCCAAGTTACTCAAACCCTAGCAAGTTTCATAGCTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGTCAAATCCCGGAGTTTAATTCCAACTTGCCCATCTTGCCTCTCTCCAAAGCCTTGGA
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                                                                                                                                                                                                                                                                                                                                                                                                Sequence 684 BP; 212 A; 145 C; 149 G; 178 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                         9.0%; Score 684; DB 12; L 100.0%; Pred. No. 6.2e-195; ative 0; Mismatches 0;
SOB1; mouse
                                                                                                                                                                                                                                                                             Claim 29; SEQ ID NO 15; 53pp; English
                                                                                                                               28-AUG-2002; 2002US-0406657P
                                                                                                     28-AUG-2003; 2003US-00650249
binding protein; OBP3;
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                                                                                                                                                                                                                                       transgenic plant
stature and with
                          Arabidopsis thaliana
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Best Local Similarity
                                                   US2004045055-A1
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                                                                                                                                                                                                                                                                                361 TIGCCTCCTCTCCAAGCCTTGGAGATTACAATTCAAGCAACACTGGATTAGATTTTGGT
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               AGATGTGACTCAACCAATACTAAGTTCTGTTACTTCAATAACTATAGCCTTACTCAACCT
                                                                  CGCCATTTCTGCAAAACATGTCGTCGCTATTGGACACGTGGCGGTTCCTTGAGGAATGTT
                                                                                                                        CCTGTTGGAGGAGGCTTTAGGAGGAACAAGAAAGCAAATCCAGATCGAAATCTACGGTC
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                                                                                                                                                                                                                                                                    AACCCTAGCAAGTTTCATAGCTACGGTCAAATCCCGGAGTTTAATTCCAACTTGCCCATC
                                                                                                                                                                                                                                                                                                                       TIGCCTCCTCCCAAAGCCTTGGAGATTACAATTCAAGCAACACTGGATTAGATTTGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tranagenic plant; Dof transcription factor; ocs binding factor; plant size; plant stature; root growth; plant; gene; ds; OBF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5119
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   581;
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                                              5095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention comprises DNA sequences which confer an altered metabolic characteristic when they are expressed in a plant. The DNA sequences of the invention are useful for producing plants with an altered metabolic characteristic, such as: altered acid metabolism, alcohol metabolism, fatty acid metabolism, altered ametabolism, altered metabolism, altered ametabolism, altered amino acid metabolism, altered ester metabolism, altered amino acid metabolism, altered ester metabolism, altered stato, oxygenated terpene, or isoprenoid metabolism, altered stato), oxygenated terpene, or isoprenoid metabolism, altered stato), oxygenated terpene, or isoprenoid metabolism, altered stato). The DNA sequences of the invention may be used to provide disease resistance in a plant and gene building or sexual PCR procedures. The present nucleic acid represents a DNA sequence of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel genes that confer altered metabolic characteristics in Nicotiana benthamiana plants, useful for altering the levels of metabolites e.g. acids, fatty acids, amino acids, carbohydrates, hydrocarbons and sterols.
                                                                                                                                                                                                                                                                                                    Plant DNA sequence which confers altered metabolic characteristic #7187.
                                                                                                                                                                                                                                                                                                                                                                                                                                          quinone metabolism; disease resistance; gene shuffling; sexual PCR; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Miller BA;
AACGAGGAATACACATCATGGGGAGGTAACAGTTCTTGGACCGGTTTCACCTCCAACAAC
                                              AACGAGGAATACACATCATGGGGAGGTAACAGTTCTTGGACCGGTTTCACCTCCAACAAC
                                                                                                                                                                                                                                                                                                                              altered metabolic characteristic; plant; acid metabolism; alcohol metabolism; fatty acid metabolism; branched fatty acid metabolism; alkaloid metabolism; anno acid metabolism; ester metabolism; glyceride metabolism; phenolic metabolism; carbohydrate metabolism; sterol metabolism; terpene metabolism; isoprenoid metabolism; alkene metabolism; alkyne metabolism; hydrocarbon metabolism; ketone metabolism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pell RJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Blakeslee B, Mccreary DA, Pell R
Reddy AS, Shukla V, Larrinua I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 645 BP; 186 A; 151 C; 141 G; 167 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 7187; 2576pp; English.
                                                                                                                      TCAACAGGCCATCTCTCATTCTAA
                                                                                                     TCAACAGGCCATCTCTCATTCTAA
                                                                                                                                                                                                              BP.
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(DOWC ) DOW AGROSCIENCES LLC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-AUG-2002; 2002WO-US027884
                                                                                                                                                                                                              645
                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                              standard; DNA;
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Crosley R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-313091/30
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7.7%; Score 581; DB 10; Length 645; 100.0%; Pred. No. 3.7e-164;

Query Match Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                    306 AACCCTAGCAAGTTTCATAGCTACAGTCAAATCCCGGAGTTTAATTCCAACTTGCCCATC
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                      ATGGTGGAACGTGCTCGGATCGCAAAAGTCCCATTGCCTGAAGCAGCTCTAAATTGCCCT
                                                                                                  66 AGATGTGACTCAATACTAAGTTCTGTTACTTCAATAACTATGGCCTTACTCAACCT
                                                                                                                                                                                                                                                                          186 CCTGTTGGAGGAGGCTTTAGGAGGAACAAGAGCAAATCCAGATCGAAATCTACGGTC
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4232 ATGGTGGAACGTGCTCGGATCGCAAAGTCCCATTGCCTGAAGCAGCTCTAAATTGCCCT
                                                                           4292 AGATGTGACTCAACCAATACTAAGTTCTGTTACTTCAATAACTATAGCCTTACTCAACCT
                                                                                                                                                         CGCCATTTCTGCAAAACATGTCGTCGCTATTGGACACGTGGCGGTTCCTTGAGGAATGTT
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Reuber TL, Creelman RA, Pineda O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIGGIGCAAICTICAAACGCGTIAIATCCATIACIAGAAGG 4812
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ds; transcription factor; transgenic plant; growth seed germination rate; plant vigor; seedling vigor.
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19-WOV-2001; 2001US-0336049P.
11-DEC-2001; 2001US-0338692P.
14-UTN-2002; 2002US-00171468.
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Jiang C, Reube
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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Pilgrim ML,
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ADI44304 standard; DNA; 795 BP

22-APR-2004 (first entry)

ADI44304;

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                                                                                                                                                                                                                                                                                          The invention relates to a number of isolated Arabidopsis thaliana cDNA sequences and their encoded proteins which are especially transcription factor related cDNA's and proteins. The isolated or recombinant plant transcription factor polymuclectides and polypeptides are useful in producing transgenic plants with commercially valuable properties, i.e. modified or altered desirable traits as compared to a reference plant, such as an alteration in a plant growth characteristic, e.g. growth rate, germination rate of seeds, vigor of plants and seedlings, or leaf and flower sensecence. Sequence information related to the polymucleotides and polypeptides can also be used in bioinformatic search methods. The transgenic plant is useful for growing a progeny plant from a parent plant. This sequence represents one of the cDNAs of the invention.
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                                                                                                                  New plant transcription factor polynucleotides and polypeptides, useful in producing transgenic plants with commercially valuable properties, such as an alteration in a plant growth characteristic, e.g. growth rate
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Best Local Similarity 100.0%; Pred. No. 3.5
Matches 581; Conservative 0; Mismatches
                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 406; 454pp; English.
                                                2003-248221/24.
                                                                          P-PSDB; ADD30378
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The invention describes a transgenic plant comprising a recombinant polynucleotide of any one of more than 500 nucleotide sequences fully cleffined in the specification or its complement. The method of the invention can be used to produced a plant having altered traits such as: chanced tolerance to abiotic stress; glyphosphate tolerance; hormone sensitivity; disease resistance; sugar sensitivity or later flowering; altered flower structure, change in stem bifurcations, altered branching pattern, reduced apical dominance, reduced trichome density; lack of trichomes; reduced escropic trichome development; altered trichome tevelopment; increased root growth; increased root hairs; altered stem morphology; increased root growth; increased root hairs; altered development; altered call proliferation or call differentiation, rapid development; premature sensecence; increased necrosis; increase in seedling or plant size; leaf morphology; seed morphology; seed biochemistry; increase in root anthocyanins; increase in plant
                                                                                                                      transgenic; plant; enhanced tolerance to abiotic stress; glyphosphate tolerance; hormone sensitivity; disease resistance; sugar sensing; flowering; flower structure; stem bifurcation; branching pattern; apical dominance; trichome; stem morphology; root growth; root hair; seed development; cell proliferation; cell differentiation; premature senescence; necrosis; plant size; leaf morphology; seed morphology; seed biochemistry; root anthocyanin; plant anthocyanin; light response; shade avoidance; bioinformatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Haake V;
Keddie J, Broun PE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New transgenic plant comprising a recombinant polynucleotide of any or of more than 500 nucleotide sequences, useful in bioinformatic search
                                                                                         Plant transcription factor related polynucleotide #1741.
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Creelman RA, Ratcliffe O, Adam LJ, Reuber TL,
Pilgrim ML, Dubell AN, Pineda O, Yu G;
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RIECHMANN J L.
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HEARD J E.
HEARE V.
CREELMAN R A.
RATCLIFFE O.
ADAM L J.
REUBER T L.
KEDDIE J.
KEDDIE J.
FERDIE J.
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PINEDA O.
YU G.
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(YUGG/)
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(KEDD/)
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GORLACH J.

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anthocyanins, or alteration in light response or shade avoidance. Transgenic plant, polymucleotides and polypeptides are useful in bioinformatic search methods. This sequence represents a plant transcription factor related polymucleotide.
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                                                                               Length 795;
                                                        Sequence 795 BP; 236 A; 180 C; 175 G; 204 T; 0 U; 0 Other;
                                                                             Query Match 7.7%; Score 581; DB 12; Length 7 Best Local Similarity 100.0%; Pred. No. 3.5e-164; Matches 581; Conservative 0; Mismatches 0; Indels
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                                                                                          Best Local Similarity ....
Matches 581; Conservative
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The invention relates to Arabidopsis thaliana nucleic acid sequences. The DNA sequences and the polypeptides they encode are useful for identifying homologous or related genes, for producing compositions that modulate the expression or function of the polypeptides, for mapping functional compositions that could be protein, in diagnosis, for studying associated complete the strains that are capable of various plant strains to determine the strains that are capable of withstanding a particular disease or environmental stress, for enhancing or inhibiting production of blosynthetic products in plants and to create genetically modified and transgenic organisms, such as plant cells and plants. Transgenic plants are useful for introducing or improving disease resistance and stress tolerance in plants, screening biologically active agents, such as functioned and insecticides, and for elucidating blochemical pathways. Sequences ABX5649-ABX55647 represent Arabidopsis thaliana collumn part of the printed specification but was obtained in electronic format directly from USPTO at sequence data for this patent collumn.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yu Y;
To Haas WD;
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Ledford BL, Woessner
Davis KR, Allen K,
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Pred. No. 5.9e-163;
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Garcia CA, Kricker M, Slater T,
Hurban P;
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WOESSNER J P.
HAAS W D.
GARCIA C A.
AN Y.
HAMILTON C M.
                                           PRICE J L.
RAINES T M.
YU Y.
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MATHEW A V.
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SLATER T.
DAVIS K R.
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Rameaka JG,
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(RAIN/)
(YUYY/)
                                                                                                                 (RAME/)
(PAGE/)
(MATH/)
(LLEDF/)
(WOES/)
(HAAS/)
(GARC/)
(GARC/)
(GARC/)
(GARC/)
(HURE/)
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                    (HAMI/)
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GGGGT 5165 GGGGT 240	ATATC 5225 ATATC 300	ATCTT 5285 ATCTT 360	.rgrrr 5345 .rgrrr 420	GAATT 5405 GAATT 480	CAATT 5465 CAATT 540		
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GCACTAGCTATTCTTG/ 	GAGTTATTGCTGAGGA 	aaaggaaaggtatggt aaaggaaagg	AGTATGTTTATTGGTTC 	attggctatatataga(attggctatatataga(TTTTTGTGTGTTCATT TTTTTGTGTTCATT	CATTGAGACATCTATA 	, 07:17:46
AICTCTCATTCTAAGTACTCAGCACTAGCTATTCTTGATGATTCTTTGTTGGTTG	GTACATTGGTGCTTGTCATGCGAGTTATTGCTGAGGAAGATCAAACCATGCAGCTATATC	CAAAGGCTAATTTTTGAGGCTCAAAGGAAAGGTATGGTTATAAAACTATCTTTTTGATCTT 	ttaaaagatcttcaaagtgtgagtatgtttattggttggcttctggtggatatttatgttt 	TATTAGAATTTTGGTCTTATATATAGGCTATATATAGAGGTGTGGGGGGGTGATATGTATG	CAAGAGTIGAIGTIGGAAACTITTITIGIGIGITCATIGAATAATCATCGAATTCTCAATT 	TCTTGGAGACCCATTATGAGACATTGAGACATCTATA 	Search completed: December 31, 2005, 07:17:46 Job time : 2705 secs
5106 ATC 181 ATC	5166 GTP 241 GTP	5226 CM 301 CM	5286 TTA 361 TTA	5346 TAT 421 TAT	5406 CM 481 CM	5466 TCT 541 TCT	pleted: 2705 g
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Arabidopsis thaliana DNA chromosome 3, BAC clone T22E16.
AL132975
                                                                 AX405124 Sequence
AX643977 Sequence
AX044091 Sequence
AX044091 Sequence
AX03511 PRT100 DNA
X05868 Plasmid pRT
AR75401 Sequence
AX275254 Sequence
AX275254 Sequence
BD209863 Improved
BD209860 Improved
BD209861 Improved
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Burect Submission

Burect Submission

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Buchemited (23-FBB-2000) MIPS, at the Max-Planck-Institut fuer

Buchemite, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail:

Buchemite, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail:

Buchemite, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail:

Coordinator: Marcel Salanoubat and Francis Queiter, Groupement

Gaston Cremieux, BP191, 91006 Evry Cedex, France;

http://www.genoscope.cns.fr

Information on performance of analysis and a more detailed

annotation of this entry and other sequences of chromosomes 3, 4

and 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/thal/.
                          CS007934 Sequence
CS025573 Sequence
AJ524488 Arabidops
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AY234328 Binary ve
AY456904 Binary ve
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AX275255 Sequenc
A51131 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note="overlap to BAC T26112 (EMBL:AL132954)"
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Arabidopsis thaliana
                          CS007934
CS025573
AXT405124
AR643977
AX044091
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AX026717
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SOURCE
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AUTHORS
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ATT22E16
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AJ616346 Nicotiana
AJ616346 Nicotiana
AP65911 Tobacco r
AY788908 N-termina
AY737283 C-termina
AY737283 C-termina
AY234330 Binary ve
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AF218466 Activatio
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              GenCore version
Copyright (c) 1993 - 2005
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Gapop 60.0 , Gapext 60.0
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7580
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Perfect score:
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LSWPSKLDEIKSKFEKISGLPNCCGAIDITHIVMNLPAVEPSNKVWLDGEKNFSMTLQ
AVVDPDMRFLDVIAGWPGSLNDDVVLKNSGFYKLVEKGKRLNGEKLPLSERTELREYI
                                                                                                                                                                                                                                                                                                                                      /translation="MGPIKTIKKKKRAEKKVDRNVLLAATAAATSASAAAALNNNDDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VGDSGFPLLPWLLTPYQGKPTSLPQTEFNKRHSBATKAAQMALSKLKDRWRIINGVYM
MPDRNRLPRIIPVCCLLHNIIIDMEDQTLDDQPLSQQHDMYYRQRSCKLADEASSVLR
                                                                                                                                                                                                                                                                                                                                                                           DDSSSQSLDWWDGFSRRIYGGSTDPKTFESVFKISRKTFDYICSLVKADFTAKPANFS
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                                                 note="similarity to predicted proteins, Arabidopsis
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gene="T22E16.20"
complement(join(3660. .3728,3821. .4575,5038. .5077,
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Gene="T22E16.30"
join(10334. .11042,11136. .11350)
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/gene="T22E16.20"
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/gene="T22E16.20"
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5262. .5330))
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Contains Prokaryotic membrane lipoprotein lipid attachment site AA164-174"

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4081 AATTAGTACAAATTATGTTAATATGCAGCAAGGGAACCAACATCAGCTAGAATGTGTCAC 4140 10312 AATTAGTACAAATTATGTTAATATGCAGCAAGGAAACCAACATCAGCTAGAATGTGTCAC 10371	AACTGACCAGAACCCTAATAATTACTTACGGCAGCTCTCATCACCACCCGACTTCTCAGGT	TGCAGGTTCGAGTCAAGCTAGAGTGAATTCAATGGTGGAACGTGCTCGCATCGCAAAAGT	CCATTGCCTGAAGAGCTCTAAATTGCCCTAGATGTGACCCAACCAA	TTACTTCAATAACTATAGCCTTACTCAACCTCGCCATTTCTGCAAAACATGTCGTCGTCA 4380 	81	GAGAAGCAAATCCAGATCTACGGTCGTGGTCTCGACTGATAATACTACTACTAC		AATCCCGGAGTTTAATTCCAACTTGCCCATCTTGCCTCTCCAAAGCCTTGGAGATTA 4620	4680	4740		ATTACTAGAAGGTAAGGAAGGTGTTAATCAAGGGATTCTCAACAGAAGAAGTAGTC 	TICCAATCACTAATGITTAAGCCCTTGATGGATTTTTCTTCAGGGGGTTAGGGCCAC	GCAACAAAAAATGTGAAGGCGGAAGAATGATCAGGATCGGGGTAGGGATGGGATGG 498	GCHACLAIGHAIG GAAGCCCGAAGAGTAACAACAACAACAGGAACGAACGAAC	OY 5041 GGRATACACATCATGGGGAGGTAACAGTTCTTGGACCGGTTTCACCTCCAACAACTCAAC 5100 11272 GGAATACACATCATGGGGAGGTAACAGTTCTTGGACCGGTTTCACCTCCAACAACTCAAC 11272 GGAATACACATCATGGGGAGGTAACAGTTCTTGGACCGGTTTCACCTCCAACAACTCAAC 11331	S101 AGGCCATCTCATTCTAAGTACTCAGCACTAGCTATTCTTGATGATTCTTTGTTGGTT 5160 AF

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Weigel,D., Blazquez,M.A., Borevitz,J., Christensen,S.K.,
Fankhauser,C., Ferrandiz,C., Malancharuvil,B.J., Neff,M.M.,
Nguyen,J.T., Sato,S., Xia,Y., Wang,Z., Dixon,R.A., Harrison,M.J.,
Lamb,C.J., Yanofsky,M.F. and Chory,J.
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Activation tagging vector pSK1074
other sequences; artificial sequences; vectors.

1 (bases 1 to 10450)
Weigel,D., Ahn,J.H., Blazquez,M.A., Borevitz,J.O.,
Christensen,S.K., Fankhauser,C., Ferrandiz,C., Kardailsky,I.,
Malancharuvil,E.J., Neff,M.M., Nguyen,J.T., Sato,S., Wang,Z.,
Xia,Y., Dixon,R.A., Harrison,M.J., Lamb,C.J., Yanofsky,M.F. and
Activation tagging in Arabidopsis
Plant Physiol. 122 (4), 1003-1013 (2000)
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/nocte=nr-DNA left border"
8064. .8749
/note="includes mannopine synthase promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (122-DEC-1999) Plant Biology Laboratory, Institute for Biological Studies, 10010 N. Torrey Jolla, CA 92037, USA Location/Qualifiers
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hote="from cauliflower mosaic virus 35S 4270. .4294 /note="T-DNA right border"
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/function="confers kanamycin resistance"
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/product="neomycin phosphotransferase"
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/note="derived from pUC19"
1662. .2204
/note="derived from phage f1"
2663. .2829
/note="derived from pUC19"
2830. .2849
/note="from T7 RNA polymerase"
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Activation tagging vector pSKI074,
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Pax:81-45-503-9586)
An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al. (1998) Plant J. 15:707-720; Seki et al. (2002) Secience 296:141-145).
This clone is in a modified pBluescript vector.
Please visit our web site (http://rarge.gsc.riken.jp/) for further
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1. .1457
/organism="Arabidopsis thaliana"
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/db_xref="taxon:3702"
/chromosome="3"
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100.0%; Pred. No. 0;
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/note="common name: thale
                                                                                                                                                                                                                                                                                                clone="RAFL25-48-C17"
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/gene="At3g55370"
134. .1105
/gene="At3g55370"
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Arabidopsis thaliana gene for zinc finger protein OBP3, complete cds, clone: RAFL25-48-C17.
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Arabidopsis thaliana (thale cress)
Arabidopsis thaliana (streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                 GAATCCGAGGAGGTTTCCCCGATATTACCCTTTGTTGAAAAGTCTCAATAGCCCTCTGGTC
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Nicotiana tabacum
Nicotiana, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamiids; Solanales; Solanaceae; Nicotiana.
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Submitted (05-DEC-2003) Huang C.Y., School of Molecular &
Biomedical Science, The University of Adelaide, The University of
Adelaide, South Australia, 5005 Adelaide, AUSTRALIA
Location/Qualifiers
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                                               124 GTCGTGCTCCACCATGTTGGGGATCTAGATATCACATCAATCCACTTGCTTTGAAGACGT
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Simple and complex nuclear loci created by newly transferred chloroplast DNA in tobacco
Proc. Natl. Acad. Sci. U.S.A. 101 (26), 9710-9715 (2004)
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'note="chloroplast DNA of pPRV111A"
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/mol_type="genomic DNA"
/cultivar="Petit Havana (N, N)"
/db_xref="taxon:4097"
/note="krl integrant"
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/note="neoSTLS2 sequence"
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/note="neoSTLS2 sequence"
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Yamada T., Tanaka, Y. and Kasumi, T.
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Published Only in DataBase (1999)
2 (bases 1 to 2939)
2 (bases 1 to 2939)
2 wamada, T., Tanaka, Y. and Kasumi, T.
Direct Submission
Submitteed (03-SEP-1998) Tetsuji Yamada, Okayama University, Faculty
St. Agriculture; Tsushima Naka 1-1, Okayama, Okayama 700-8530, Japan (E-mail:tdry@cc.okayama.u.ac.jp, Tel:81-86-251-8307,
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     121 ACTGAAACCATGCATAATCTCTCAAGTCTCAACCTATGAAGAATCATGTAACCAATAGAC 180
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                                       5943 TATCATCATGATTAGTTAATGCATGATCTATAATGTATTTCTTTGAACATAGATATGTCAT
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tive 0; Mismatches 0; Indels 0
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/mol_type="genomic DNA"
/cultivar="Bright Yellow"
/cultivar="taxon:4097"
/clone="Tentativaly names as S-5"
/cell_type="Suspension cultures"
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Submitted (08-AUG-2001) MCDB, Yale University, 165 Prospect Street,
New Haven, CT 06520, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               238 radecriricerriardecaardardecarricaradaadeccarcrirerracracretic 179

    .9663
/organism="Tobacco rattle virus RNA2-based VIGS vector

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    178 TTTCGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGGTTTCCCGATATTACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           358 AGATATCACATCAATCCACTTGCTTTGAAGACGTGGTTGGAACGTCTTTTTTCCACGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTTGTTGAAAAGTCTCAATAGCCCTCTGGTCTTCTGAGACTGTATCTTTGATATTCTTGG
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Tobacco rattle virus RNA2-based VIGS vector pTRV2
other sequences; artificial sequences; vectors.

1 (bases 1 to 9663)
Liu,Y., Schiff,M., Marathe,R. and Dinesh-Kumar,S.P.
Tobacco Ratl, EDS1 and NPR1/NIM1 like genes are required for Plant J. 30 (4), 415-429 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 4462;
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Best Local Similarity 100.0%; Pred. No. 5.2e-148;
Matches 332; Conservative 0; Mismatches 0;
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                                                                                                                                        'product="beta lactamase"
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/db_xref="taxon:188057"
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2606. .3466
/gene="amp"
2606. .3466
/gene="amp"
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AF406991/c
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Use of a gateway compatible vector for transient plant transfection
Unpublished
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LTTYVKNWHRFPAFTHILARLMNAHEFRMAMVOGELVINGSVHDCYTFFHEQTETF
SSIMSEYHDDFRQFLHIYSQDVACYGENLAYPPKGFTEMMFFVSANPNVSFTSPDLNV
ANMDNFFAPVFTMGKYYTQGBKVLMPLAQVHANCDGFHVGRMLNELQQYCDEWQGG
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KVSRELYPVVHIGDESWRMYTTDMASVPVSVIGEEVADLSHRENDIKNAINLMFWGI"
                                                                                                                                                                                                                                                                                                                                                                                                                 circular SYN 27-MAR-2003
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GERMANY
                                                                                                              6430 TITGITGAAAAGICICAAIAGCCCTCTGGTCTTCTGAGACTGIAICTTTGAIAITCTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amp gene; beta lactamase; cat gene; cdB gene; chloramphenicol acetyl transferae; control of cell death B protein. Transfection vector pBTdest Transfection vector pBTdest other sequences; artificial sequences; vectors.
     6370 TTTCGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGGTTTCCCGATATTACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jakoby, M.J.

Direct Submission

Submitted (26-MAR-2003) Jakoby M.J., Salamini, MPI for F
Submitted (26-MAR-2003) Jakoby M.J., Salamini, MPI for F
Submitted (26-MAR-2003)

Breeding Research, Carl-von-Linne Weg 10, 50829 Koeln, C
Location/Qualifiers
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product=-control of cell death B protein"
protein id="CADB3081.1"
db_xref="GI:29335744"
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/mol_type="other DNA"

/db_xref="taxon:225975"

31. .443

A0te="355"

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421. .424

/note="355"

/note="atk1"

689. .1348
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/note="attR2"
2168. .2463
/gene="nosT"
2168. .2463
/gene="nosT"
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/gene="ccdB"
1690. .1995
/gene="ccdB"
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689. .1348
/gene="cat"
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C-terminal TAP T-DNA vector pYL436, complete sequence.
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Liu, Y. and Dinesh-Kumar, S.P.
Direct Submission
Submitted (28-AUG-2004) MCDB, Yale University, New Haven, CT 06520, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6430 TITGITGABARGICICAATAGCCCTCTGGTCTTCTGAGACTGTATCTTGATATTCTTGG 6489
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C-terminal TAP T-DNA vector pYL436
other sequences; artificial sequences; vectors.
1 (bases 1 to 1267)
Rubio,V., Shen,Y., Saijo,Y., Liu,Y., Gusmaroli,G.,
Dinesh-Kumar,S.P. and Deng,X.W.
An alternative tandem affinity purification strategy applied harabidopsis protein complex isolation
Plant J. 41 (5), 767-778 (2005)
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Liu, Y. and Dinesh-Kumar, S.P.
A C-terminal tandem affinity purification (TAP) T-DNA vector
Unpublished
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                                                                                                                                                                                                                                                                                                                                                Length 12537;
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                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                             780. .844.
/note="TMV UI omega sequence"
/sefs. .1231
/note="2x protein A IgG binding domain"
1256. .1279
/note="protease 3C cleavage site"
                                          /note="duplicated CaMV 35S promoter"
                                                                                                                                                                                                                                                                                                                                                Query Match
4.4%; Score 332; DB 11; L
Best Local Similarity 100.0%; Pred. No. 4.3e-148;
Matches 332; Conservative 0; Mismatches 0;
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/note="NOS terminator"
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/note="9x myc tag"
1704. .3577
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/note="6x HIS tag"
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AY737283.1 GI:52630860
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N-terminal TAPa T-DNA vector pN-TAPa, complete sequence.
AY788908
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N-terminal TAPa T-DNA vector pN-TAPa
other sequences; artificial sequences; vectors.
1 (bases 1 to 12537)
Rubio, V., Shen, Y., Saijo, Y., Liu, Y., Gusmaroli, G.,
Dinesh-Kumar, S.P. and Deng, X.W.
An alternative tandem affinity purification strategy applied Marabidopsis protein complex isolation
Plant J. 41 (5), 767-778 (2005)
                                                                                                                                                                                                                                                                                                                                                          Gaps
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Rubio, V. and Deng, X.W.

Direct Submission

Submitted (21-00T-2004) MCDB, Yale University, 165, Prospect
New Haven, CT 06511, USA

Location/Qualifiers
/note="Tobacco rattle virus RNA2-based T-DNA vector
synonym: pYL156"
1. .1639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .12537
/organism="N-terminal TAPa T-DNA vector pN-TAPa"
/mol_type="other DNA"
/db xref="texcn:300483"
/note="derived from pPZP222"
                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                 4.4%; Score 332; DB 11; Length 9663;
100.0%; Pred. No. 4.5e-148;
tive 0; Mismatches 0; Indels 0
                                                                                                   1640. .1708
/note="multiple cloning site region"
1709. .2133
/note="TYN strain ppk20 RNA2 3'-sequence"
2104. .2154
/note="synthetic sequence"
2155. .8894
/note="pCambia 0390 sequence"
8895. .9663
/note="CAMV 35S promoter from pCASS2"
                                                                                                                                                                                                                                                                                                                                                                                             6190 AGATATCACATCAATCCACTTGCTTTGAAGACGTGGTTGGAACGTCTTCT
                                                                                 'note="TRV strain ppk20 RNA2 5'-sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGTAGACGAGAGTGTCGTGCTCCACCATGTTG 6521
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Best Local Similarity 100.0
Matches 332; Conservative
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AY788908/c
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/translation="MGPERRPADIRRATEADMPAVCTIVNHYIETSTVNFRTEPQEPQ
EWTDDLVKLKERYFWLVAEVDGEVAGIAYAGPWKARNAYDWTAESTVYVSPHYGKTGL
GSTLYTHILKSLEAQGFKSVVAVIGLPNDPSVRMHEALGYAPRGMLRAAGFKHGNWHD
VGFWQLDFSLPVPPRPVLPVTEI"
                                                                                                                                                                                                                                                                                                                                    /note="synonym: pat; bialaphos/phosphinothricin resistance gene from Streptomyces hygroscopicus; similar to GenBank Accession Number X17220"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1231. 1332. Anotes multiple cloning site from vector pBlueSfi AB in GenBank Accession Number AF327874" 1333. 1935 Anotes region from nopaline-type Ti plasmid CSB of Agrobacterium tumefaciens in GenBank Accession Number X07435"
                                                          /organism="Binary vector pLH7500"
/mol type="other DNA"
/db xref="taxon:226216"
6. .424
/note="promoter/chhancer sequence from the 35S gene of Cauliflower mosaic virus in GenBank Accession Numbers X05868 and V00140"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1013. .1212
/notes-terminator sequence from the 35S gene of
Cauliflower mosaic virus in GenBank Accession Numbers
XOSB68 and V00140"
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evidence=experimental
replace=""
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/evidence=experimental
/replace="a"
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evidence=experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="phosphinothricin acetyl transferase"
/protein_id="AAO85365.1"
/db_xref="GI:29569731"
                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="confers resistance to bialaphos and phosphinothricin"
                                                                                                                                                                                                                                                                         note="putative transcription start site"
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/note="right flanking T-DNA border"
1425. .1437
/note="repeat C'".
  Geilweilerhof, Siebeldingen 76833, Germany
Location/Qualifiers
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/replace=""
1460. 11471
/note="repeat C"
/rpt type=inverted
1485. 1495
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
/transl_table=
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392. .398
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Binary vector pLH7500
Binary vector pLH7500
chbr sequences, artificial sequences; vectors.

1 (bases 1 to 8903)
Hausmann, L. and Toepfer, R.
Development of Plasmid Vectors
Conversion of Custom-ralloked RAPE VARIETIES: 155-172;
GPZ e. V., Von Sieboldstr. 8, Goettingen, Germany (1999)
Hausmann, L. and Toepfer, R.
Hausmann, L. and Toepfer, R.
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                       1. 12607
/organism="C-terminal TAP T-DNA vector pYL436"
/ord_type="other DNA"
/db_xref="taxon:293967"
/note="derived from pPZP222"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.4%; Score 332; DB 11; Length 12607;
100.0%; Pred. No. 4.3e-148;
tive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                         845. .2718
/note="attR1-CmR-ccdB-attR2 GATEWAY cassette"
2752. .3009
                                                                                                                    1. .769
/note="duplicated CaMV 35S promoter"
                                                                                                                                                                                                                                                                                                                                    1181. .3204
/note="protease 3C cleavage site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8903 bp DNA Binary vector pLH7500, complete sequence. AY234331
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                                                                                                                                                             780. .844
/note="TMV Ul omega sequence"
                                                                                                                                                                                                                                                                                                                                                                             3244. .3591
/note="zx 1gG binding domain"
3670. .3932
/note="Nos terminator"
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                                                                                                                                                                                                                                                                   'note="9x myc tag"
3163. .3180
'note="6x HIS tag"
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Matches 332; Conservative
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RDWAAVREDQPLTVVGIDRPTIDRDVKAIGRRDFVVIDGAPQAADLAVSAIKAADFVL
IPVQPSPYDIWATADLVELVKQRIEVTDGRLQAAFVVSRAIKGTRIGGEVAEALAGYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /trānslation="wphywrngrlarrkrlgclpalqwhwnpqargigysgrkpsgpy
oigaalgddlyeklkaaqaaqrqribaarapgeswqaaadrirkesrqppaagapsir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="partitioning protein ParA encoded by parA of plasmid pVS1; similar to F plasmid SopA in GenBank Accession Number X04619, RKZ IncC in GenBank Accession Number L27758, and Pl ParA in GenBank Accession Number L27758,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6430 TITGITGAAAAGICTCAATAGCCCTCTGGICTTCTGAGACTGTATCTTTGATATTCTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     276 TGTTCCTCGTGGGGGGGTCCATCTTTGGGACCACTGTCGTAGAGGCATCTTGAACGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  156 TITICGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGTTTCCCGATATTACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6190 AGATATCACATCAATCCACTTGCTTTGAAGACGTGGTTGGAACGTCTTCTTTTCCACGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6310 TAGCCTTTCCTTTATCGCAATGATGGCATTTGTAGAAGCCATCTTCCTTTTCTACTGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LPILESRITQRVSYPGTAAAGTTVLESEPEGDAAREVQALAAEIKSKLI"
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4.4%; Score 331; DB 11; L
Best Local Similarity 100.0%; Pred. No. 1.4e-147;
Matches 331; Conservative 0; Mismatches 0;
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Binary vector pLH7000, complete sequence.
AY234330
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                                                                                                                                                                                                                                                                                                                                                                                                       /protein_id="AAO85367.1"
/db_xref="G1:29569733"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein_id="AA085368.1"
db_xref="GI:29569734"
evidence=experimental
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/transl_table=11
/product="ParA"
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/transl_table=11
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                                 replace="c'
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AY234330/c
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VERSION
KEYWORDS
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Trrdrafelarmidhirpgdovtvtrildrarstrdildiaeriqeagagirslera
Dtttpagravijvyegagagiaepersiildrirsgereaakkagvkegpepijtpagiahar
Elidoegrivkeaaaligvhrstlyralerseevtptearrkgafredalteadalaa
Aenerqeeqa"
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3273. .3278
3295. .3295
3309. .3995
/note="resolvase-like protein encoded by park of plasmid
pVS1; similar to Tn3 resolvase in GenBank Accession Number
V00613, Tn917 resolvase in GenBank Accession Number
M1180, and RK2 ParA in GenBank Accession Number
/codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3116. .6887
/note="origin of replication and partitioning region from plasmid pVS1 of Pseudomonas; similar to GenBank Accession Number U10487; serves as origin of replication in Agrobacterium tumefaciens host" /evidence=experimental
                                                                                                                                                                                                                                                                                                                                                                                           ornithine cyclodeaminase gene
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/evidence=experimental
/replace="c"
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/note="compared to GenBank Accession Number J01749"
/evidence=experimental
/replace="gta"
2912
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/evidence=experimental
                                                                                                                                                  to GenBank Accession Number X07435"
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                                                                                                                                                                                                                                                                                                                                                      complement (1545. .1935)
/note="3" sequence of the ocd; non-functional"
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/protein_id="AAO85366.1"
/db_xref="GI:29569732"
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/replace="c"
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/replace=""
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2193
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   /rpt_type=inverted
1512. 1522
/note="repeat B"
/rpt_type=inverted
: 1517
                                                                                                                                                         note="compared
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/note="synonym: pat; bialaphos/phosphinothricin resistance
gene from Streptomyces hygroscopicus; similar to GenBank
Accession Number X17220"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="phosphinothricin acetyl transferase"
/protein_id="AAO85360.1"
/db_xref="d1:25569725"
/translation="MGPERRPADIRRATEADMPAVCTIVNHYIETSTVNFRTEPQEPQ
BYDDLVWLERRRYPHIVAEDGEFKOUGEVAGIAYAGPMKARNAYDWTAESTVYVSPRHQRTGL
GSTLYTHLIKSLEAGOFKSVVAVIGLPNDPSVRWHEALGYAPRGMLRAAGFKHGNWHD
VGFWQLDFSLPVPPRPVLPVTEI"
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/note="right border region from nopaline-type Ti plasmid
C58 of Agrobacterium tumefaciens in GenBank Accession
Number X07435."
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/note="multiple cloning site from vector pBlueSfi BA in
GenBank Accession Number AF327875"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="promoter/enhancer sequence from the 35S gene of Cauliflower mosaic virus in GenBank Accession Numbers X05868 and V00140"
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/note="terminator sequence from the 35S gene of
Cauliflower mosaic virus in GenBank Accession Numbers
X05868 and V00140"
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/evidence=experimental
/replace=""
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/evidence=experimental
/replace="a"
1386. -1409
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/evidence=experimental
                                                                                                                                        (in) Brauer, D., Roebbelen, G. and Toepfer, R. (Eds.);
BIOENGINEBRING OF CUSTOM-TAILORED RAPE VARIETIES: 155-172;
BIOENGINEBRING OF CUSTOM-TAILORED RAPE VARIETIES: 155-172;
Chases 1 to 8911)
Hausmann, L. and Toepfer, R.
Birct Submission
Submitted (12-FEB-2003) Institute for Grapevine Breeding Geilweilerhof, Sisbeldingen 76833, Germany
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="confers resistance to bialaphos and phosphinothricin"
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Binary vector pLH7000
Binary vector pLH7000
other sequences; artificial sequences; vectors.
( bases 1 to 8911)
Hausmann, L. and Toepfer, R.
Development of Plasmid Vectors
                                                                                                                                                                                                                                                                                                                                                             1. .8911
/organism="Binary vector pLH7000"
/mol_type="other DNA"
/db_xref="taxon:226215"
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transl_table=11
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misc_feature
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/note="resolvase-like protein encoded by park of plasmid by81; similar to Tn3 resolvase in GenBank Accession Number V00613, Tn917 resolvase in GenBank Accession Number M11100, and RKZ ParA in GenBank Accession Number L27758"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /trānslation="MNKSAAAGLLGYARVSTDDQDLTNQRAELHAAGCTKLFSEKITG
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ELIDQEGRTVKRAAALLGVHRSTLYRALERSEEVTPTEARRGAFREDALTEADALAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3124. .6895
/note="origin of replication and partitioning region from plasmid pv81 of Peeudomonas; similar to GenBank Accession Number UI0487; serves as origin of replication in Agrobacterium tumefaciens host"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ornithine cyclodeaminase gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="compared to GenBank Accession Number X07435" /evidence=experimental /replace="t" | 1944. .3108 /note="colEl origin of replication sequence of pBR322; similar to GenBank Accession Number J01749; serves as origin of replication in Escherichia coli host" /evidence=experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                               /evidenceexperimental
/replace="a"
complement(1553, .1943)
/note="3' sequence of the ornithine cycloneord, non-functional"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="original nucleotide changed to destroy a SfiI
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"note="compared to GenBank Accession Number J01749"
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                                                                                                           GenBank Accession Number X07435"
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O
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1439
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transT_table=
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-10_signal
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                                                                                                                                        circular SYN 10-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1388. .1990
/note="right border region from nopaline-type Ti plasmid
C58 of Agrobacterium tumefaciens in GenBank Accession
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence from the 35S gene of
in GenBank Accession Numbers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1060. .1259
/notes-terminator sequence from the 35S gene of
Cauliflower mosaic virus in GenBank Accession Numbers
XOSS68 and V00140"
                                                                                                                                                                                                                                                                         cother sequences; artificial sequences; vectors.

1 (bases 1 to 8958)

S Haummann, L. and Toepfer, R.

Development of Plasmid Vectors

(in) Brauer, D., Roebbelen, G. and Toepfer, R. (Eds.);

BIOBNGINEERING OF CUSTOM-TAILORED RAPE VARIETIES: 155-172;

GPZ e. V., VON Sieboldstr. 8, Goettingen, Germany (1999)

E 2 (bases 1 to 8958)

S Hausmann, L. and Toepfer, R.

Direct Submission

C Submitted (12-FEB-2003) Institute for Grapevine Breeding Gellweilerhof, Siebeldingen 76833, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="compared to GenBank Accession Number X05868"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8958 bp DNA
Binary vector pLH5000, complete sequence.
AY234327
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         1286. .1387
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                                                                                                                                                                                                                                           Binary vector pLH5000
Binary vector pLH5000
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misc_feature
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misc_feature
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SOURCE
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                                                                                                           /note="nucleotide changed to conserve palindromic sequence following Sfil restriction site-destruction" /evidence=experimental /replace="9"
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/note="partitioning protein ParB encoded by parB of plasmid pVS1; similar to F plasmid SopB in GenBank Accession Number X04619, RK2 KorB in GenBank Accession Number L27758, and PI ParB in GenBank Accession Number L27758.
                                                                                                                                                                                                                                                                                                                                            4302. .4931
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plasmid pVS1; similar to F plasmid SopA in GenBank
Accession Number X04619, RKZ IncC in GenBank Accession
Number L27758, and Pl ParA in GenBank Accession Number
                                                                                                                                                                                                /note="original nucleotide changed to destroy two SfiI restriction sites"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6190 AGATATCACATCAATCCACTTGCTTTGAAGACGTGGTTGGAACGTCTTTTTTCCACGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5198. .5210
/note="identical to the korB operator binding site of
plasmid RK2 in GenBank Accession Number L27758.1"
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                                                         4147. .4179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="AAO85363.1"
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4237. 4242
4258. 4263
4291. 4298
restriction site"
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Best Local Similarity
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-10_signal
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                                                             stem_loop
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LPILESRITQRVSYPGTAAAGTTVLESEPEGDAAREVQALAABIKSKLI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OIGAALGDDLVEKLKAAQAAQRQRIEAEARPGESWQAAADRIRKESRQPPAAGAPSIR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KQKDDLVETCIRLNTTHVAMQRTKKAKNGRLVTVSEGEALISRYKIVKSETGRPEYIE
IELADWMYREITEGKNPDVLTVHPDYFLIDPGIGRFLYRLARRAAGKAEARWLFKTIY
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                 DTTTPAGRMYLTVFAGIABFERSLI I DRTRSCREAAKARGVKFÖPRPTLTPAQI AHAR
EL I DQBGRTYKEAAALLGVHRSTLYRALERSEBVTPTEARRRGAFREDALTEADALAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          translation="MPHVWRNGRLARRKRLGCLPALQWHWNPQARGIGVSGRKPSGPV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ERSGSAGEFKKFCFTVRKLIGSNDLPEYDLKEEAGQAGPILVMRYRNLIEGEASAGS"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5245. .5257
Inote="identical to the korB operator binding site of plasmid RK2 in GenBank Accession Number L27758.1"
5305. .6480
/note="partitioning protein ParB encoded by parB of plasmid pVS1, similar to F plasmid SopB in GenBank Accession Number X04619, RK2 KorB in GenBank Accession Number and Pl ParB in GenBank Accession Number ParB in GenBank Accession Number Forts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="partitioning protein ParA encoded by parA of plaemid pVS1; similar to F plaemid SopA in GenBank Accession Number X04619, RKZ IncC in GenBank Accession Number X0758, and Pl ParA in GenBank Accession Number
                                                                                                                                                                                                                                                                                                                                                                                      /note="original nucleotide changed to destroy two Sfil restriction sites"
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                                                                                                                   /note="original nucleotide changed to destroy a SfiI
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4.4%; Score 331; DB 11; L
Best Local Similarity 100.0%; Pred. No. 1.4e-147;
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                                                                                                                                                                                                                     4194. .4226
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4284. .4289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MNKSAAAGLLGYARVSTDDQDLTNQRAELHAAGCTKLFSEKITG
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/note="origin of replication and partitioning region from forth: origin of replication and partitioning region from Jabamid pVS1 of Pseudomonas; similar to GenBank Accession Number UI0487; serves as origin of replication in Agrobacterium tumefaciens host"
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/note="resolvase-like protein encoded by parR of plasmid
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similar to GenBank Accession Number J01749; serves as
origin of replication in Escherichia coli host"
/evidence=experimental
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/replace="a"
1433. .1456
/note="right flanking T-DNA border"
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/note="3' sequence of the ocd; non-functional"
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1540. .1550
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1567. 1577
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1572
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1413
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Search completed: December 31, 2005, 14:03:29 Job time: 24339 secs

111, Appl 112, Appl 112, Appl 31, Appl 30, Appl 5254799 30, Appl 52, Appl 14, Appl 14, Appl 14, Appl 14, Appl 11, Appl 11, Appl 11, Appl 12, Appl 14, Appl 16, Appl 17, Appl 18, Appl 18, Appl 19, Appl 19, Appl 11, Appl 11, Appl 11, Appl 11, Appl 12, Appl 13, Appl 14, Appl 16, Appl 17, Appl 18, Appl 18, Appl 19, Appl 1

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Searched:

Database

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323 CATCAATCCACTTGCTTTGAAGACGTGGTTGGAACGTCTTTTTTCCACGATGTTCCTC
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                                                                                                                                                                                                                                                      Sequence 30,
Patent No. 529
Sequence 35,
Sequence 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3.9%; Score 299; DB 3; Length 323; 100.0%; Pred. No. 7.8e-104; ive 0; Mismatches 0; Indele
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| Sequence 46, Application US/10012070A
| Sequence 46, Application US/10012070A
| Patent NO. 6867293
| GENERAL INFORMATION:
| APPLICANT: Hawkes, Timothy
| APPLICANT: Marner, Simon
| APPLICANT: Marner, Simon
| APPLICANT: Bachoo, Sarvinder
| APPLICANT: Bachoo, Sarvinder
| APPLICANT: Bickerill, Andrew
| TITLE OF INVENTION: Herbicide Resistant Plants
| FILE REFERENCE: 50490/UST
| CURRENT APPLICATION NUMBER: US/10/012,070A
| CURRENT APPLICATION NUMBER: PCT/GB00/01573
| PRIOR APPLICATION NUMBER: PCT/GB00/01573
| NUMBER OF SEQ ID NOS: 57
| SOFTWARE: Patentin Ver. 2.0
| SEQ ID NO 46
| LENGTH: 323
US-09-577-424-1

US-09-528-819-11

US-09-528-819-12

US-09-528-819-12

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US-08-446-486-31

US-08-466-318-30

US-08-466-30

US-08-463-308-31

US-08-463-308-31

US-09-363-30-30

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US-09-458-093-2

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US-08-458-093-2

US-08-458-093-2

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US-08-458-083-1

US-08-458-1

US-08-488-270-1

US-08-488-270-1

US-08-810-70-1
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Best Local Similarity 100.
Matches 299; Conservative
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Sequence 1, Appli
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./cgn2 6/ptodata/1/ina/PE_COMB.seq:*
./cgn2 6/ptodata/1/ina/PE_COMB.seq:*
./cgn2 6/ptodata/1/ina/PE_COMB.seq:*
./cgn2 6/ptodata/1/ina/RE_COMB.seq:*
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                                    GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-330-770-1
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US-09-469-211A-19/C

Sequence 19, Application US/09469211A

Parent No. 6660524

GENERAL INFORMATION:

APPLICANT: J. Turck

APLICANT: J. Archer

TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN EUKARYOTES

FILE REFERENCE: 9341-021

CURRENT APPLICATION NUMBER: US/09/469,211A

CURRENT FILING DATE: 1999-12-22

PRIOR APPLICATION NUMBER: UK 9828660.2

PRIOR APPLICATION NUMBER: UK 9828660.2

PRIOR PILING DATE: 1998-12-44

NUMBER OF SEQ. DD NOS: 19

SOFTWARE: PatentIn Ver. 2.1
            Sequence 1, Application US/09353332

Patent No. 6316697

GENERAL INFORMATION:
APPLICANT: Dixon, Richard A.
APPLICANT: AND, Christopher
TITLE OF INVENTION: CONSTITUTIVE DISEASE RESISITANCE (CDR1)
TITLE OF INVENTION: GENE AND METHODS OF USE THEREOF
FILE REFERENCE: SALK2820-1
CURRENT APPLICATION NUMBER: US/09/353,332
CURRENT FILING DATE: 1999-07-14
EARLIER FULING DATE: 1998-07-14
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PASESEQ for Windows Version 4.0
IENGTH: 4839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 3.7%; Score 281; DB 3; Length 4839; Best Local Similarity 100.0%; Pred. No. 3.4e-97; Matches 281; Conservative 0; Mismatches 0; Indels
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ORGANISM: Artificial Sequence
FEATURE:
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; LOCATION: (1111)...(2421)
US-09-353-332-1
US-09-353-332-1/c
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LENGTH: 470
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Sequence 3 Application US/09810861B

Patent No. 6770799

GENERAL INFORMATION:

APPLICANT: Mor, Tasfrir S.

APPLICANT: Mor, Charles J.

APPLICANT: Mason, Hugh S.

TITLE OF INVENTION: EXPRESSION OF RECOMBINANT HUMAN ACETYLCHOLINESTERASE IN TITLE OF INVENTION: EXPRESSION OF PROMINANT PLICANTION WIMBER: US/09/810, 861B

CURRENT PILING DATE: 2001-03-16

PRIOR FILING DATE: 2000-03-17

NUMBER OF SEQ ID NOS: 5

SOFTWARRE: PatentIN Ver. 3.1

SEQ ID NO 3

LENGTH: 5767
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; OTHER INFORMATION: Description of Artificial Sequence:chimaeric; ; OTHER INFORMATION: promoter US-09-469-211A-19
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Best Local Similarity 100.0%; Pred. No. 1.2e-74;
Matches 222; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 7.9e-75;
tive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 222; Conservative
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US-09-810-861B-3/c
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US-09-042-426-1/C
is Sequence 1, Application US/09042426
; Patent No. 6114608
; GENERAL INFORMATION:
; APPLICANT: ITVIN J. Mettler, Paul S. Dietrich, Ralph Sinibaldi
; TITLE OF INVENTION:
; TITLE OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6114608artis Corporation
; "TETTLE OF MORTIS AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 2728;
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STATE: New Jersey
COUNTRY: USA
ZIP: 07901
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Parentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/042,426
FILING DATE: MATCH 11, 1998
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.9%; Score 221; DB 3; 100.0%; Pred. No. 2.1e-74; tive 0; Mismatches 0;
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 44 0 200.7 (Germany)
FILING DATE: 10-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Kurf G Briscoe
REGISTATION NUMBER: 33,141
RECESTRATION NUMBER: 33,141
RELECHONISICATION INFORMATION:
TELECHONE: (914) 332-1700
TELECHONE: (914) 332-1844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Hoxie, Thomas
REGISTRATION NUMBER: 32,993
REFERENCE/DOCKET NUMBER: 135/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8614
                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2728 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 221; Conservative
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                                  Sequence 4, Application US/09810861B

Sequence 4, Application US/09810861B

Patent No. 6770799

GENERAL INFORMATION:
APPLICANT: Mor, Teafrir S.
APPLICANT: Mored, Hermona
APPLICANT: Arntzen, Charles J.
APPLICANT: Manner, Hugh S.
TITLE OF INVENTION: TRANSGENIC PLANTS
FILE REFERENCE: BT1-45
CURRENT APPLICATION NUMBER: US/09/810,861B
CURRENT PILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/190,440
PRIOR APPLICATION NUMBER: 60/190,440
PRIOR APPLICATION NUMBER: 60/190,440
PRIOR APPLICATION NUMBER: 3.01
SOFTWARE: Patentin Ver. 3.1

SOFTWARE: Patentin Ver. 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature; LOCATION: (11862)..(12157); DOTEN INFORMATION: Description of Artificial Sequence: plasmid vector; OTHER INFORMATION: pTW036. Identity of sequence residues 11862-12157 unknown. US-09-810-8618-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13991 TCTTGAACGATAGCCTTTCCTTTATCGCAATGATGGCATTTGTAGAAGCCATCTTCCTTT 13932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6420 GATATTACCCTTTGTTGAAAAGTCTCAATAGCCCTCTGGTCTTCTGAGACTGTATCTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6360 TCTACTGTCCTTTCGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGGTTTCCC
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Patent No. 6063988
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
NUMBER OF SEQUENCE AND ITS USE
NUMBER OF SEQUENCES:
CORRESPONDENCE A.
CORRESPONDENCE A.
COUNTRY: Tarrytown
STATE: New York
COUNTRY: U.S.A.
ZIP: 10591-5144
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB storage
COMPUTER Gateway 2000
COMPUTER: Gateway 2000
COMPUTER: Microsoft Windows 98
CURRATION NUMBER: US/08/836,402B
FILING DATE: 02-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
2.9%; Score 222; DB 3; L
Best Local Similarity 100.0%; Pred. No. 6.7e-75;
Matches 222; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Artificial Sequence
                           JS-09-810-861B-4/C
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US-08-836-402B-7/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 14446
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Gaps

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TTTCGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGGTTTCCCGATATTACCC 6429
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GENERAL INFORMATION:
APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi
TITLE OF INVENTION: DNA CONStruct Containing Bacillus
NUMBER OF SEQUENCES: 11
CORRESPONDENCES: ADDRESS:
ADDRESSEE: No. 6229075artis Corporation
STREET: 564 Morris Avenue
                                                                                                                                                                                                                                                                                                                  ..
                                                                                                                                                                                                                                                                     2.3%; Score 175; DB 3; Length 532;
99.3%; Pred. No. 7.9e-57;
tive 0; Mismatches 2; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/330,760
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTTGTTGAAAAGTCTCAATAGCCCTCTGGTCTTCTGA 6466
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PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/042,426
FILING DATE: March 13, 1998
ATTORNEY/AGENT INFORWATION:
NAME: HOAXIE, THOMAS
REGISTRATION NUMBER: 32,993
REFERENCE/DOCKET NUMBER: 135/1
TELEPHONE: (919) 541-8614
TELEPHONE: (919) 541-8619
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/09330760
Patent No. 6229075
                                                                                                                     MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: 35S Promoter
US-09-291-238-1
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 312 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 99.39
Matches 275; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Summit
STATE: New Jersey
COUNTRY: USA
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Sequence 1, Application US/09291238
Patent No. 6222104
GENERAL INFORMATION:
APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi TITLE OF INVENTION: DNA Construct Containing Bacillus NUMBER OF SEQUENCES:
ADDRESSEE: No. 6222104artis Corporation
STREET: S64 Morris Avenue
CITY: Summit
STATE: New Jersey
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                                                                                                                                                                                                                                                                                                          Length 532;
                                                                                                                                                                                                                                                                                                                                                   2; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/291,238
FILING DATE:
                                                                                                                                                                                                                                                                                                          Score 175; DB 3;
Pred. No. 7.9e-57;
                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION NUMBER: 09/042,426
FILING DATE: March 13, 1998
ATTORNEY/AGENT INFORMATION:
NAME: HOASIG, THOMBER: 32,993
REFERENCE/DOCKET NUMBER: 135/1
TELEPHONE: (919) 541-8614
TELEPHONE: (919) 541-8614
      TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 532 base pairs
TYPE: nucleic acid
STRANDEDNES: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                            Query Match 2.3%;
Best Local Similarity 99.3%;
Matches 275; Conservative (
                                                                                                                                                                                                   ; ANTI-SENSE: NO; IMMEDIATE SOURCE: ; CLONE: 35S Promoter US-09-042-426-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 8
US-09-291-238-1/c
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TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHATICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: 355 Promoter
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STREET: 564 Morris Avenue
CITY: Summit
STATE: New Jersey
LENGTH: 532 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                           Query Match
Best Local Similarity 99.34
Matches 275; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 532 base pairs
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                        ; CLONE: US-09-328-473-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6370 TTTCGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGGTTTCCCGATATTACCC 6429
                                                                                                                                                                                                                                                                                                                                                                                                                                                 229 TGTTCCTCGTGGGTGGGGGCTCCATCTTTGGGACCACTGTCGGTAGAGGCATCTTGAACGA 170
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                                                                                                                                                                                                                                                                                                                                                          289 AGATATCACATCACATTGCTTTGAAGACGTGGTTGGAACGTCTTTTTTCCACGA
                                                                                                                                                                                                                                                                                             Gaps
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5 Sequence 1, Application US/09328473

7 Patent No. 6232533

7 GENERAL INFORMATION:

APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi

7 TITLE OF INVENTION: DNA CONStruct Containing Bacillus

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 6232533artis Corporation
                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                2.3%; Score 175; DB 3; Length 532; 99.3%; Pred. No. 7.9e-57;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 07901

COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: PRESENT PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/328,473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49 ITTGTTGAAAGTCTCAATAGCCCTCTGGTCTTCTGA 13
                                                                                                                                                                                                                                                                                          0; Mismatches
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CLASSIFICATION
FILING APPLICATION DATA:
RPLICATION DATA:
APPLICATION DATA:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: HOxie, Thomas
REGISTRATION NUMBER: 32,993
REPRENCE/DOCKET NUMBER: 135/1
TELECOMMUNICATION INFORMATION:
TELEPRONE: (919) 541-8614
TELEPRONE: (919) 541-8614
INFORMATION FOR SEC ID NO: 1:
SEQUENCE CHARACTERISTICS:
                 LENGTH: 532 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: 355 Promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 564 Morris Avenue CITY: Summit STATE: New Jersey COUNTRY: USA
                                                                                                                                                                                                                                                                     Best Local Similarity 99.3
Matches 275, Conservative
    SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                            US-09-330-760-1
                                                                                                                                                                                                                                                    Query Match
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6250 IGITCCTCGTGGGGGGGGCCATCTTTGGACACCACTGTCGGTAGACGCATCTTGAACGA 6309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            109 TITCGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGGTTTCCCGATATTACCC 50
                                                                                                                                                                                                                                                                                            6190 AGATATCACATCAATCCACTTGCTTTGAAGACGTGGTTGGAACGTCTTCTTTTCCACGA
                                                                                                                                                                                                                                                                                                                                                           289 AGATATCACATCAATCCACTTGCTTTGAAGACGTGGTTGGAACGTCTTCTTTTCCACGA
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                                                                                                                                                                          Gaps
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18-09-30-30-70-1/c

18-09-30-70-1/c

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                                            Score 175; DB 3; Length 532;
Pred. No. 7.9e-57;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/330,737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTTGTTGAAAAGTCTCAATAGCCCTCTGGTCTTCTGA 13
2.3%; Scor.
99.3%; Pred. No. ...
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: March 13, 1998
ATTORNEY AGENT INFORMATION:
NAME: Hoxie, Thomas
REGISTRATION NUMBER: 135/1
TELEPHONE: (919) 541-8614
TELEPHONE: (919) 541-8614
INFORMATION FOR SEG ID NO: 1:
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Gaps

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TAGCCTTTCCTTTATCGCAATGATGGCATTTGTAGAAGCCATCTTCCTTTTCTACTGTCC 6369
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VES-09-330-7144-1/c

VES-09-330-7144-1/c

Sequence 1, Application US/09330714A

Patent No. 6342660

GENERAL INCRMATION

GENERAL INCRMATION: D. Mettler, Paul S. Dietrich, Ralph Sinibaldi

APPLICONT: Irvin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi

TITLE OF INVENTION: DNA Construct Containing Bacillus

Thuringlensis Gene
                                                                                                                                                                                                             Length 532;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49 TTTGTTGAAAAGTCTCAATAGCCCTCTGGTCTTCTGA 13
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ADDRESSEE: No. 6342660artis Corporation
                                                                                                                                                                                                             Score 175; DB 3;
Pred. No. 7.9e-57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/330,714A
FILING DATE: 11-Jun-1999
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/042,426
FILING DATE: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 135/1
                                                                                                                         CLONE: 35S Promoter
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Hoxie, Thomas
REGISTRATION NUMBER: 32,993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 07901
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                 TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS
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STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
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Matches 275; Conservative
                                                                                                          IMMEDIATE SOURCE:
                                                                                                                                                                        US-09-329-169-1
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Patent No. 6329575
GENERAL INFORMATION:
APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi
TITLE OF INVENTION: DNA Construct Containing Bacillus
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
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ZIP: 07901

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMBUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/09/329,169
FILING DATE: 09-Jun-1999
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                        Length 532
                                                                                                                                                                                                                                                                2; Indels
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STREET: 564 Morris Avenue
CITY: Summit
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                      Score 175; DB 3;
Pred. No. 7.9e-57;
                                                                                                                                                                                                                                                                  0; Mismatches
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Hoxie, Thomas
REGISTRATION NUMBER: 32,993
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      TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: 355 Promoter
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Best Local Similarity 99.3%;
Matches 275; Conservative (
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US-09-329-169-1/c
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6370 TTTCGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGGTTTCCCGATATTACCC 6429
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Sequence 1, Application US/09289170

Patent No. 6573438

GENERAL INFORMATION:
APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi
TITLE OF INVENTION: DNA CONStruct Containing Bacillus
NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6573438axtis Corporation
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                                                                                                                                                                                                                                                                  2.3%; Score 175; DB 3; Length 532;
99.3%; Pred. No. 7.9e-57;
tive 0; Mismatches 2; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/289,170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: No. 6573438artis Corporation
STREET: 564 Morris Avenue
CITY: Summit
STATE: New Jersey
                                           TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHERICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: 35S Promoter
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/042,426
FILING DATE: March 13, 1998
ATTORNEY/AGENT INFORMATION:
NAME: HOXIE, Thomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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REGISTRATION NUMBER: 32,993
REFERENCE/DOCKET NUMBER: 13
TELECOMMUNICATION INFORMATION:
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (919) 541-8614
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 532 base pairs
                                                                                                                                                                                                                                                                                                                      Matches 275; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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US-09-289-170-1/c
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                                                                                                                                                                                                                                                                                                                           Gaps
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TITLE OF INVENTION: DNA Construct Containing Bacillus
NUMBER OF SEQUENCES: 11
CORRESPONDENCE DESS:
ADDRESSEE: No. 6399860artis Corporation
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                                                                                                                                                                                                                                                                    Length 532;
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: DATENTIN PC compatible

COPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIN Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/328,826

FILING DATE: 09-Jun-1999

CLASSIFCATION COMPAN:

APPLICATION NUMBER: US/09/042,426

FILING DATE: MARCH 13, 1998

ATTORREY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                         6190 AGATATCACATCAATCCACTTGCTTTGAAGACGTGGTTGGAACGTCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49 TTTGTTGAAAAGTCTCAATAGCCCTCTGGTCTTCTGA 13
                                                                                                                                                                                                                                                                  2.3%; Score 175; DB 3;
99.3%; Pred. No. 7.9e-57;
tive 0; Mismatches 2,
                                                                                                                                        IMMEDIATE SOURCE:
CLONE: 35S Promoter
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: HOXIE, Thomas
REGISTRATION NUMBER: 32,993
REFERENCE/DOCKET NUMBER: 135/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 564 Morris Avenue
CITY: Summit
STATE: New Jersey
COUNTRY: USA
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TELEFAX: (919) 541-8689
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Patent No. 6399860
GENERAL INFORMATION:
                                              TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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SEQUENCE CHARACTERISTICS:
LENGTH: 532 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                         Best Local Similarity 99.3
Matches 275; Conservative
                                                                                                                         ANTI-SENSE: NO
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6249
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229 IGTTCCTCGTGGGTGGGGGTCCAICTTTGGGACCACTGTCGGTAGAGGCAICTTGAACGA 170
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                                                                                                          Query Match 2.3%; Score 175; DB 3; Length 532; Best Local Similarity 99.3%; Pred. No. 7.9e-57; Matches 275; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                6430 TITGITGAAAAGTCTCAATAGCCCTCTGGTCTTCTGA 6466
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
MATT-SENSE: NO
IMMEDIATE SOURCE:
CLONE: 35S Promoter
US-09-289-170-1
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Search completed: December 31, 2005, 19:14:53 Job time : 843 secs

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RESULT 2
US-11-038-981A-5/c
US-11-038-981A-5/c
; Sequence 5, Application US/11038981A
; Publication No. US20050283856A1
; GENERAL INFORMATION:
; APPLICANT: COnner, Timothy W.
; APPLICANT: Plasinski, Stanislaw
; APPLICANT: Pang, Sheng Z
US-10-508-263-122/c
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                                                               December 31, 2005, 07:17:49; Search time 469 Seconds (without alignments) 8472.606 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpna/USO8_NEW PUB. seq:*
2: /cgn2_6/ptodata/1/pubpna/USO8_NEW PUB. seq:*
2: /cgn2_6/ptodata/1/pubpna/USO7_NEW PUB. seq:*
4: /cgn2_6/ptodata/1/pubpna/DST_NEW PUB. seq:*
5: /cgn2_6/ptodata/1/pubpna/USO7_NEW PUB. seq:*
7: /cgn2_6/ptodata/1/pubpna/USO1_NEW PUB. seq:*
7: /cgn2_6/ptodata/1/pubpna/USO1_NEW PUB. seq:*
8: /cgn2_6/ptodata/1/pubpna/USO1_NEW PUB. seq:*
9: /cgn2_6/ptodata/1/pubpna/USO1_NEW PUB. seq:*
9: /cgn2_6/ptodata/1/pubpna/USO1_NEW PUB. seq:*
10: /cgn2_6/ptodata/1/pubpna/USO1_NEW PUB. seq:*
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Compugen Ltd.
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US-11-038-981A-5
US-11-038-981A-10
US-10-391-414-10
US-11-038-981A-20
US-11-038-981A-25
US-11-038-981A-25
US-11-038-981A-25
US-11-038-981A-26
US-11-038-981A-27
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US-11-038-981A-27
US-11-038-981A-15
                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
           GenCore version
(c) 1993 - 2005
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                                               nucleic search, using sw model
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Gapop 60.0 , Gapext 60.0
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US-10-16-76-22
US-10-10-516-76-81
US-11-071-651-11
US-11-038-981A-12
US-11-038-981A-12
US-11-038-981A-10
US-11-038-981A-10
US-11-038-981A-10
US-11-038-981A-10
US-11-038-981A-10
US-11-038-981A-10
US-10-995-561-56237
US-10-995-561-56237
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US-11-117-187-192
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                                                                    APPLICATE BASE Plant Science GmbH
TITLE OF INVENTION: Constructs and methods for regulating gene expression FILE REFERENCE: 53262-20085.00
CURRENT APPLICATION NUMBER: US,10/508,263
CURRENT FILING DATE: 2004-09-20
NUMBER OF SEQ ID NOS: 126
SOFTWARE: Patentin Ver. 2.1
LENGTH: 11667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGGGTTTCCCGATATTACCCTTTG
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99.3%; Pred. No. 1.1e-27;
tive 0; Mismatches 1;
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Sequence 122, Application US/10508263 Publication No. US20050260754A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Artificial sequence
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US-10-391-414-10/c
US-10-391-414-10/c
Sequence 10, Application US/10391414
Publication No. US20050278799A1
GENERAL INFORMATION:
APPLICANT: KATSURA, Koji
APPLICANT: ITO, Yusuke
TITLE OF INVENTION: Stress Induced Promoter Derived From Rice
FILE REFERENCE: 382.1041
CURRENT APPLICATION NUMBER: US/10/391,414
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Publication No. US20050283856A1

GENERAL INFORMATION:

APPLICANT: Conner, Timothy W.

APPLICANT: Flasinski, Stanislaw

APPLICANT: Pang, Sheng Z

PRICANT: Solidation Stanish Sheng Z

PRICANT: Solidation Stanish Sheng Z

PRICANT: Solidation NUMBER: US/11/038,981A

PRICANT FILING DATE: 2005-01-20

PRICANT APPLICATION NUMBER: 60/537,793

PRICANT APPLICATION NUMBER: 60/537,793

PRICANT STANISH SPECTION NUMBER: Solidation Stanish Sheng SPECTION NUMBER: Solidation NU
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APPLICANT: You, Jinsong
TITLE OF INVENTION: CHIMERIC PROMOTERS FOR USE IN PLANTS
FILE REFERENCE: 38-21(51446) B
CURRENT APPLICATION NUMBER: US/11/038,981A
CURRENT FILING DATE: 2005-01-20
PRIOR APPLICATION NUMBER: 60/537,793
PRIOR PADPLICATION NUMBER: 60/537,793
NUMBER OF SEQ ID NOS: 35
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LENGTH: 332
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Sequence 18, Application US/11038981A

Publication No. US20050283856A1

GENERAL INFORMATION:

APPLICANT: Conner, Timothy W.

APPLICANT: Flasinski, Stanislaw

APPLICANT: Pang, Sheng Z

APPLICANT: You, Jinsong

TITLE OF INVENTION: CHIMERIC PROMOTERS FOR USE IN PLANTS

FILE REFERENCE: 38-21(51446)B

CURRENT PEPLICATION WUMBER: 20/5-01-20

PRIOR FILING DATE: 2004-01-20

PRIOR FILING DATE: 2004-01-20

WUMBER OF SEQ ID NOS: 35

LENGTH: 1273
                                                                                                                                                                                                                                                                                                      Query Match 0.8%; Score 62; DB 6; Length 835; Best Local Similarity 100.0%; Pred. No. 4.1e-14; Matches 62; Conservative 0; Mismatches 0; Indels
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US-11-038-981A-20/c

i Sequence 20, Application US/11038981A

i Publication No. US20050283856A1

i GENERAL INFORMATION:

i APPLICANT: Conner, Timothy W.

i APPLICANT: Flasinski, Stanislaw

APPLICANT: Pang, Sheng Z

i APPLICANT: Pang, Sheng Z

i TITLE OF INVENTION: CLIMERIC PROMOTERS FOR USE IN PLANTS

TITLE OF INVENTION: USHREIC PROMOTERS FOR USE IN PLANTS

FILE REFERENCE: 38-21(51446)B

; CURRENT APPLICATION NUMBER: US/11/038,981A
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0.8%; Score 62; DB 7; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.9e-14;
Matches 62; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Artificial promoter sequence US-11-038-981A-18
                                  2002-377316
                                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Cauliflower mosaic virus
US-10-391-414-10
CURRENT FILING DATE: 2003-03-18
PRIOR APPLICATION NUMBER: JP 2005.
PRIOR FILING DATE: 2002-12-26
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Artificial Sequence
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6190 AGATATCACATCCACTTGCTTTGAAGACGTGGTTGGAACGTCTTCTTTTTCCACGA 6249
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; Sequence 26, Application US/2050283856A1
; Publication No. US20050283856A1
; General INNORMATION:
; APPLICANT: Conner, Timothy W.
; APPLICANT: Palinski, Stanislaw
; APPLICANT: Pang, Sheng
; TITLE OF INVEXTION: CHIMERIC PROMOTERS FOR USE IN PLANTS
; TITLE OF INVEXTION: CHIMER: US/11/038,981A
; CURRENT APPLICATION NUMBER: US/11/038,981A
; CURRENT PILING DATE: 2005-01-20
; REID RAPPLICATION NUMBER: 60/537,793
; PRIOR FILING DATE: 2004-01-20
; NUMBER OF SEQ ID NOS: 35
; SEQ ID NO 26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1935;
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Publication No. US20050283856A1
GENERAL INFORMATION:
APPLICANT: Conner, Timothy W.
APPLICANT: Plasinski, Stanislaw
APPLICANT: Pang, Sheng Z
APPLICANT: Pang, Sheng Z
APPLICANT: CHU, Jinsong
TITLE OF INVENTION: CHIMERIC PROMOTERS FOR USE IN PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 7; Le 3.7e-14;
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0.8%; Score 62; DB 7; Le
Best Local Similarity 100.0%; Pred. No. 3.7e-14;
Matches 62; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Artificial promoter sequence
US-11-038-981A-25
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 0.8%; Score 62; DB Best Local Similarity 100.0%; Pred. No. 3.7 Matches 62; Conservative 0; Mismatches
CURRENT APPLICATION NUMBER: US/11/038,981A CURRENT FILING DATE: 2005-01-20 PRIOR APPLICATION NUMBER: 60/537,793 PRIOR FILING DATE: 2004-01-20 NUMBER OF SEQ ID NOS: 35 SEQ ID NO 25 LENGTH: 1935
                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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ORGANISM: Artificial Sequence
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US-11-038-981A-24/C
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                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Artificial promoter sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Artificial promoter sequence
                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 0.8%; Score 62; DB Best Local Similarity 100.0%; Pred. No. 3.9 Matches 62; Conservative 0; Mismatches
CURRENT FILING DATE: 2005-01-20
PRIOR APPLICATION NUMBER: 60/537,793
PRIOR FILING DATE: 2004-01-20
NUMBER OF SEQ ID NOS: 35
SEQ ID NO 20
LENGTH: 1273
TYPE: DNA
ORGANISM: Artificial Sequence
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Publication No. US20050283856A1
GENERAL INFORMATION:
APPLICANT: Conner, Timothy W.
APPLICANT: Plasinski, Stanislaw
APPLICANT: Paginski, Stanislaw
APPLICANT: Paginski, Stanislaw
APPLICANT: You, Jinsong
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Matches 62; Conserv
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US-11-038-981A-25/c
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US-11-038-981A-19/C
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TITLE OF INVENTION: CHIMERIC PROMOTERS FOR USE IN PLANTS
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                                                                                                                                                                                   TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                     0.8%;
                                                                                                                                                                                                                                                                                                                          Best Local Similarity 100.0
Matches 62; Conservative
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                                                                                                                                                               LENGTH: 1963
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                                                                                                                                                                                                                                                                                   0.8%; Score 62; DB 7; Length 1939;
100.0%; Pred. No. 3.7e-14;
tive 0; Mismatches 0; Indels
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0.8%; Score 62; DB 7; Length 1963;
Best Local Similarity 100.0%; Pred. No. 3.7e-14;
Matches 62; Conservative 0; Mismatches 0; Indels
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| Sequence 27, Application US/11038981A
| Publication No. US20050283856A1
| Publication No. US20050283856A1
| CENERAL INFORMATION:
| APPLICANT: Flashiski, Stanislaw
| APPLICANT: Flashiski, Stanislaw
| APPLICANT: Pang, Sheng Z
| APPLICANT: Pang, Jinsong
| TITLE OP INVENTION: CHIMERIC PROMOTERS FOR USE IN PLANTS
| TILE OP INVENTION: ABPLICATION NUMBER: US/11/038,981A
| CURRENT APPLICATION NUMBER: US/11/038,981A
| PRIOR PILING DATE: 2005-01-20
| PRIOR FILING DATE: 2004-01-20
| NUMBER OF SEQ ID NOS: 35
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                                                                                                                                                                                                              , OTHER INFORMATION: Artificial promoter sequence US-11-038-981A-24
FILE REPERENCE: 38-21(51446)B
CURRENT APPLICATION NUMBER: US/11/038,981A
CURRENT FILING DATE: 2005-01-20
PRIOR APPLICATION NUMBER: 60/537,793
PRIOR FILING DATE: 2004-01-20
NUMBER OF SEQ ID NOS: 35
LENGTH: 1939
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; Sequence 28, Application US/11038981A
; Publication No. US20050283856A1
; GENERAL INFORMATION:
; APPLICANT: Conner, Timothy W.
; APPLICANT: Plasinski, Stanislaw
; APPLICANT: Pang, Sheng Z
; APPLICANT: You, Jinsong
                                                                                                                                                               TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                       Best Local Similarity 100.0
Matches 62; Conservative
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LENGTH: 1963
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Sequence 23, Application US/11192801

Publication No. US20050273882A1

GENERAL INFORMATION:

APPLICANT: Romano, Charles P.

TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants

FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
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; Sequence 29, Application US/11038981A
; Publication No. US2050283856A1
; GENERAL INFORMATION:
; APPLICANT: Conner, Timothy W.
APPLICANT: Plasinski, Stanislaw
APPLICANT: Pang, Sheng Z
APPLICANT: Now. Second Second
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0.8%; Score 62; DB 7; Lu
Best Local Similarity 100.0%; Pred. No. 3.7e-14;
Matches 62; Conservative 0; Mismatches 0;
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COTHER INFORMATION: Artificial promoter sequence US-11-038-981A-28
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US-11-038-981A-29
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FILE REFERENCE: 38-21(51446)B
CURRENT APPLICATION NUMBER: US/11/038,981A
CURRENT FILING DATE: 2005-01-20
PRIOR APPLICATION NUMBER: 60/537,793
PRIOR FILING DATE: 2004-01-20
NUMBER OF SEQ ID NOS: 35
SEQ ID NO 28
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. 4,
Search completed: December 31, 2005, 20:22:35
Job'time : 470 secs
                                            LOCATION: (25)..(640)
OTHER INFORMATION: P-CaMV.35S
FRATURE:
NAME/KRY: intron
LOCATION: (669)..(1472)
OTHER INFORMATION: I-Zm.Hsp70
                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: terminator
LOCATION: (3475)..(3
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Sequence 15, Application US/11192801
Publication No. US20050273882A1
SEQUENCE 15, Application No. US20050273882A1
SEGNERAL INFORMATION:
THIS REPERENCE: 18-21(15304) Cry3Bb Improved Exp. Corn
TTILE OF INVENTION: Improved Exp. Corn
CURRENT APPLICATION WUMBER: US/11/192,801
CURRENT FILING DATE: 2005-07-29
PRIOR APPLICATION WUMBER: US/10/232,665
PRIOR APPLICATION WUMBER: US/99/377,466
PRIOR FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 15
LENGTH: 3754
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NAME/KEY: CDS
LOCATION: (1241)..(3199)
OTHER INFORMATION: Cry3Bbl variant 11231mv2
CURRENT APPLICATION NUMBER: US/11/192,801
CURRENT FILING DATE: 2005-07-29
PRIOR APPLICATION NUMBER: US/10/232,665
PRIOR PILING DATE: 2002-08-29
PRIOR PLILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 43
SEQ ITMARE: Patentin Ver. 2.0
SEQ ID NO 23
LENGTH: 3469
                                                                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY: promoter
LOCATION: (25)..(640)
OTHER INFORMATION: P-CAMV.35S
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LOCATION: (3217).. (3450)

CTHER INFORMATION: T-Ta.hsp17

US-11-192-801-23
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LOCATION: (664)..(734)
OTHER INFORMATION: L-Ta.hcbl
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NAME/KEY: intron
LOCATION: (748)..(1238)
OTHER INFORMATION: I-OS.Act1
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6190 AGATATCACATCAATCCACTTGCTTTGAAGACGTGGTTGGAACGTCTTCTTTTTCCACGA 6249
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                                                                                                                   LOCATION: (3475)...(3730)
OTHER INFORMATION: Agrobacterium tumefaciens nos 3' transcription
OTHER INFORMATION: termination and polyadenylation sequence
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LOCATION: (1490)..(3448)
OTHER INFORMATION: Cry3Bb1 variant v11231
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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.	0 0 6 4 6 6	
OM nucleic - nucleic search, using sw model	0 7 0 0	
Run on: December 31, 2005, 05:24:09; Search time 17827 Seconds (without alignments) 19893.761 Million cell updates/sec	. c 30	
Title: US-10-650-249-1 Perfect score: 7580 Sequence: 1 agctctattaattcaagagagccgccaccgcggtggagct 7580	0 0 0 0 10 0 10 0 10 0 10 0 10 0 10 0	62 0.8 62 0.8 62 0.8
Scoring table: OLIGO NUC 3 Gapext 60.0		
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Mord size € 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 44 44 5 45 45 45 45 45 45 45 45 45 45 4	
Minimum DB seq length: 0 Maximum DB seq length: 200000000		
Post-processing: Listing first 45 summaries		
Database : BST:* 1: gb_est1:* 2: gb_est2:* 3: gb_htc:* 5: gb_est4:* 6: gb_est5:* 7: gb_est6:* 9: gb_gss1:* 11: gb_gss3:*	CNSOAGOU LOCUS DEFINITION VERSION VERSION KEYWORDS SOURCE ORGANISM	CNSOAGOU A TABLIAGOBIS GSLTFB52E04 thaliana (th BX822604.1 BX822604.1 HTC; GSLT of Arabidopsis A Tablidopsis A Tablidopsis Sukaryota, V
		rogida: Pur

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	BX822604 Arabidops	CW802337 WiscDsLox	CW797151 WiscDsLox	BX822618 Arabidops	DR749973 79-L02582	DR750042 79-L02144	AL084743 Arabidops	DR750041 79-L02144	B26529 F9G12TF IGF	B97814 F18P18TFB I	AQ011657 F24E16TFB	CK437874 GQ0042.BR	AA585745 28394 Lam	AQ361597 mgxb0004F	AQ361936 mgxb0005M	CL517384 SAC3E03 F	CF854584 psMC001xM	AQ362115 mgxb0003F	BH173054 SALK 0015	T22381 4389 Lambda	BP861585 BP861585	CC966736 BOIFC82TR
SUMMARIES	ΙD	CNSOA60U	0 CW802337	0 CW797151	CNS0A5T8	DR749973	DR750042	O CNSOOPNT	DR750041	B26529	B97814	AQ011657	CK437874	AA585745	AQ361597	AQ361936	0 CL517384	CF854584	AQ362115	BH173054	T22381	BP861585	CC966736
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ALIGNMENTS

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/note="Wector: pDS-Lox; Sequence generated in the course of an Arabidopsis T-DNA tagging program. TAIL-PCR was used to generate sequencing templates that represent A.t. genomic DNA flanking the left boxder of the pDs-Lox T-DNA insert. PCR products were sequenced directly by using the p745 primer 5' AACGTCCGCAATGTGTTAITAAGTTGTC 3'"
                                                                                                                                                                                                                                         CWB02337 7480J24 Arabidopsis thaliana T-DNA insertion flanking sequences Arabidopsis thaliana genomic, genomic survey sequence. CWB02337
                                                                                                1426
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/mol_type="genomic DNA"
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/db_xref="taxon:3702"
/tisfue_type="seeds produced by primary (Basta-resistant)
transformants"
/clone_lib="Arabidopsis thaliana T-DNA insertion flanking
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Arabidopsis thaliana
Bukaryota; thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosida; eurosida II; Barssicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 736)
Woody, S.T., Monson, S.S., Jester, P.J., Austin-Phillips, S.,
Amasino, R.M., Sussman, M.R. and Krysan, P.J.
A New Community Resource for Knocking-Out Small Genes and
Tandemly-puplicated Gene Families and for Mosaic Analysis in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     537 GCCTTTCGTGAAAAATGCGCATGTTCTTGTTGGAATCTAGGAATCTTCTTCTAAAG
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GAGGCTCAAAGGAAAGGTATGGTTATAAAACTATCTTTTGATCTTTAAAAGATCTTCA
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ive 0; Mismatches 0;
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University of Wisconsin-Madison
425 Henry Mall, Madison, WI 53706,
Tel: (608) 262-4640
Email: swood/@facstaff.wisc.edu
Class: TAIL-PCR.
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Unpublished (2004)
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CW802337
LOCUS
DEFINITION
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KEYWORDS
SOURCE
ORGANISM
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AUTHORS
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                                        pnds"
                                                                                                                                                      Query Match 9.6%; Score 726; DB Best Local Similarity 99.5%; Pred. No. 0; Matches 1046; Conservative 0; Mismatches
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/note="Vector: pDS-Lox; Sequence generated in the course of an Arabidopsis T-DNA tagging program. TAIL-PCR was used to generate sequencing templates that represent A.t. genomic DNA flanking the left border of the pDs-Lox T-DNA insert. PCR products were sequenced directly by using the p745 primer 5' AACGTCCGCAATGTGTTAITAAGTTGTC 3'"
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Arabidopsis thaliana Full-length CDNA Complete sequence from clone GSLTFB532B03 of Flowers and buds of strain col-0 of Arabidopsis Exaliana (thale cress).

BX822618

BX822618

HTC; GSLT CDNA.

Arabidopsis thaliana (thale cress)
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9.4%; Score 711; DB 10; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 711; Conservative 0; Mismatches 0; Indels
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Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
I (bases I to 720)
Woody,S.T., Monson,S.S., Jester,P.J., Austin-Phillips,S.,
Amasino,R.M., Sussman,M.R. and Krysan,P.J.
A New Community Resource for Knocking-Out Small Genes and
Tandemly-Duplicated Gene Families and for Mosaic Analysis in
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                                                                     GACAAAAAATCGTTTTAGCTCTATCATCTGTCTTTTTGAAGAAAAATATCAACATATC
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/db_xref="taxon:3702"
/tisue_type="seeds produced by r
transformants"
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Biotechnology Center
University of Wisconsin-Madison
F.S. Henry Mall, Madison, WI 53706,
Tel: (608) 262-4640
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Class: TALL-PCR.
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Couractor, Costantino, Vittorioso, Davies, Gilmartin, Giraudat, Parcy, Sablowski, Coupland, Martin, Angenent, Baeumlein, Carbonero, Colombo, Tonelli, owski, Coupland, Martin, Angenent, Baeumlein, Carbonero, Colombo, Tonelli, Engstroem, Droege-Laser, Gatz, Kavanagh, Kushnir, Zabeau, Laux, Holdsworth, Ruberti, Smeekenes, Somssich, Weisshaar, Traes Research
Universitaetsstrasse 25, D-33594 Bielefeld, Germany
Email: bernd, weisshaardeni-bielefeld, Germany
Email: bernd, weisshaardeni-bielefeld, Germany
Data analysis performed in the frame of REGULATORS (Exploiting
Inter-species conservation in promoter sequences to identify
regulators of reproductive development and physiological
performance), a Trilateral Co-Operation in Plant Genomics between
Spain (WCYT), France (GENOPLANTE) and Germany (GABI) coordinated by
G. Coupland (coupland-ad-mpiz-koelln, mpg.de). Authors: Vincent
Thareau (IBP-Orsay UMR8618 CNRS-UPS, thareau-ad-ibp.u-psud.fr) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                868 bp mRNA linear EST 19-JUL-2005
79-L025823-065-006-G10-SeLA MPIZ-ADIS-065d Arabidopsis thaliana
CDNA clone 006-G10, mRNA sequence.
DR749973
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Definition of the terms used to describe the quality of the clone:
The about 2250 sequences from the clone collection were sorted according to clones and clustered. If more than one contig was formed, the clone was designated 'Contamination'. The contigs and singlerons were blasted against CDS plus pseudogenes from the TIGRv5 annotation, and the resulting AGI code is presented if more
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Paz-Ares, J., Valencia, A., Costantino, P., Vittorioso, P., Davies, B., Gilmartin, P., Giraudat, J., Parcy, F., Reindl, A., Sablowski, R., Coupland, G., Martin, C., Angenent, G.C., Bacumlein, H., Mock, H.P., Droege-Laser, W., Gatz, C., Kavanagh, T., Kushnir, S., Zabeau, M., Boux, T., Hordsworth, M., Ruberti, I., Ratcliff, F., Smeekens, S., Somssich, I., Weisshaar, B. and Traas, J.

REGIA, an EU project on functional genomics of transcription factors from Arabidopsis thaliana

Comp. Funct. Genomics 3 (2), 102-108 (2002)
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571 TTACTCAAACCCTAGCAAGTTTCATAGCTACGGTCAAATCCCGGAGTTTAATTCCAACTT
                                                                                                                                                                                                                                                        631 GCCCATCTTGCCTCCTCCCAAGCCTTGGAGATTACAATTCAAGCAACACTGGATTAGA
                                                                                                                                                                                                                                                                                                                                                  751 GGATGCATGGAGAATACCTCCATCACAACAAGCTCAGCAATTCCCTTTCTTGATCAACAC
                                                                                                                                                                                                         GCCCATCTTGCCTCCTCCCAAAGCCTTGGAGATTACAATTCAAGCAACACTGGATTAGA
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KEYWORDS
SOURCE
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The sequences are based on single pass reads.

Life Technologies (a division of Invitrogen) members carried out full-length libratiries construction : Temple G. Genoscope members carried out sequencing and annotation : Castelli V. Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach D., Salanoubat M.

URGV INRA : Clepet C., Caboche M.

Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). S prime and 3 prime are assembled with Phrap.
                                        Eukaryota; Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurocids II; Brassicales; Brassicaceae; Arabidopsis.

(bases 1 to 1371)

Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C., Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V., Temple, G., Caboche, M., Weissenbach, J. and Salanoubat, M. Whole Genome Sequence Comparisons and 'Pull-Length' cDNA Sequences: A Combined Approach to Evaluate and Improve Arabidopsis Genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4105 GCAGCAAGGGAACCAACATCAGCTAGAATGTGTCACAAACTGACCAGAACCCTAATAATTA
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100.0%; Pred. No. 0;
ive 0; Mismatches 0; Indels
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/tissue_type="Flowers and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /plasmid="pCMVSPORT_6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
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/gene="At3g55370"
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Best Local Similarity 100.0
Matches 708; Conservative
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than 90 percent identity was found. The sequences were also blasted against all TIGRv5 introns, and matches longer than 50 bp with 95 percent identity are reported as 'intron found'. The remaining terms for Sequalysis describe the outcome of the evaluation of the CDS detected after pairwise alignment with CDS plus pseudogenes from the TIGRv5 annotation file. The sequences or contigs for which a full CDS with or without STOP codon was detected, a BLASTP against all TIGRv5 protein sequences was performed. Full perfect: 100 percent identity, full good: better than 95 percent identity over more than 95 percent of the sequence; partial good: better than 95 percent of the sequence; performed the sequence; weak similarity: less than 95 percent identity over less than 95 percent of the sequence; no similarity: no hit from BLASTP. Note that the collection contains a few clones for which sequencing was not successful, which could have simple technical reasons.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /lab host="800-610"
/lab host="800-610"
/lab host="800-610"
/clone lib="MPIZ-ADIS-0654"
/clone lib="MPIZ-ADIS-0654"
/clone lib="MPIZ-ADIS-0654"
/clone servetor: pDONR201; In the context of the BU-funded project REGIA (QLG-CT11995-00876, coordinator Javier Paz-Ares), a set of transcription factor ORFs was generated. The ORFs were produced in a decentralized way in the labs of the participants. Most of the ORFs were generated by RT-PCR using cDNA from various A. thaliana tissues as a template. Initially, it was planned to use yeast recombination to move the ORFs from the Cloning vectors into target constructs. For this reason, a number of the clones contain 'REGIA tags' (RG_tag1: 5pr-ATTCCACCACC-3pr; RG_tag2: 5pr-ATTCCACCACC-3pr; RG_tag2: 5pr-ATTCCACCACC-3pr; RG_tag2: 6pr-CATGGCAATTCCCACC-3pr; During the lifetime of the project, the GATEWAY system became available and finally all ORFs were transferred into GATEWAY vectors. At the end of the REGIA project, the clones were collected as plasmid DNA. For end-sequencing at the DNA core facility of the WBIshaar), the plasmids were re-transformed into BHSADPA, arrayed into 96 well plates and new plasmid DNA was prepared. Re-transformation proved to be difficult because a number of clones are rectansformed into proved to be difficult because
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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Submitted data.

Insert Length: 868 Std Error: 0.00

Seq primer: SeLA TCGCGTTAACGCTAGCATGGATCTC.

Location/Qualifiers
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/clone="006-G10"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/ecotype="Columbia"
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Contact:

Paz.Ares, Costantino, Vittorioso, Davies, Gilmartin, Giraudat, Parcy, Sablowski, Coupland, Martin, Angenent, Baeumlein, Carbonero, Colombo, Tonelli, Engerroem, Droege-Laser, Gatz, Kavanagh, Kushnir, Zabeau, Laux, Holdsworth, Ruberti, Smeekens, Somssich, Weisshaar, Traone Research

Bielefeld University, Institute for Genome Research
Universitaetsstrasse 25, D-31594 Bielefeld, Germany
Email: bernd.weisshaarawuni-bielefeld.de
AGI: A73G55370; SegAnalysis: truncated in 5 at pos 179;
Translation: no full cds detected
Data analysis performed in the frame of REGULATORS (Exploiting inter-species conservation in promoter sequences to identify regulators of reproductive development and physiological performance), a Trilateral Co-Operation in Plant Genomics between Spain (MCYT), France (GENOPLANTE) and Germany (GABI) coordinated by G. Coupland (coupland-ad-mpiz-koeln, mpg.de). Authors: Vincent Thareau (IBP-Oreay UMR8618 CNRS-UPS, thareau-ad-ibp.u-psud.fr) and DR750042 972 bp mRNA linear EST 19-JUL-2005 79-L021445-065-006-G10-SeLB MPIZ-ADIS-065d Arabidopsis thaliana cDNA clone 006-G10, mRNA sequence. 4592 4652 4712 4772 492 lecharny-ad-ibp.u-psud.fr).
Definition of the terms used to describe the quality of the clone:
The about 2250 sequences from the clone collection were sorted
according to clones and clustered. If more than one contig was
formed, the clone was designated 'Contamination'. The contigs and Eukaryoča, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis. Paz-Ares, J., Valencia, A., Costantino, P., Vittorioso, P., Davies, Edilartin, P., Giraudat, J., Parcy, F., Reindl, A., Sablowski, R., Coupland, G., Martin, C., Angenerit, G.C., Baeumlein, H., Mock, H.P., Carbonero, P., Colombo, L., Tonelli, C., Engstroem, P., Droege-Laser, W., Gatz, C., Kavanagh, T., Kushnir, S., Zabeau, M., Laux, T., Hordsworth, M., Ruberti, I., Ratcliff, F., Smeekens, S., Somssich, I., Weisshaar, B. and Trass, J.

REGIA, an EU project on functional genomics of transcription factors from Arabidopsis thaliana
Comp. Funct. Genomics 3 (2), 102-108 (2002) ACCCTAGCAAGTTTCATAGCTACGGTCAAATCCCGGAGTTTAATTCCAACTTGCCCATCT 433 IGCCTCCTCTCCAAAGCCTTGGAGATTACAATTCAAGCAACACACTGGATTAGATTTTGGTG TGGTCTCGACTGATACTACTAGTACTTCATCACTTACTTCTCGCCCAAGTTACTCAA ACCCTAGCAAGTTTCATAGCTACGGTCAAATCCCGGAGTTTAATTCCAACTTGCCATCT 4593 TGCCTCCTCCAAAGCCTTGGAGATTACAATTCAAGCAACACTGGATTAGATTTTGGTG GAACTCAAATAAGCAACATGATAAGTGGTATGAGTTCTAGTGGTGGGTCTTGGATGCAT 493 GAACTCAAATAAGCAACATGATAAGTGGTATGAGTTCTAGTGGTGGGATCTTGGATGCAT GGAGAATACCTCCATCACAACAAGCTCAGCAATTCCCTTTCTTGATCAACACTACCGGAT 4773 IGGIGCAAICTICAAACGCGTIATATCCATTACTAGAAGG 4812 613 TGGTGCAATCTTCAAACGCGTTATATCCATTACTAGAAGG 652 Alain Lecharny (URGV-Evry UMR INRA-CNRS-UEVE, Arabidopsis thaliana (thale cress) DR750042.1 GI:71035382 Arabidopsis thaliana (bases 1 to 972) DR750042 Contact: 4533 373 4653 4713 4473 SOURCE ORGANISM RESULT 6 DR750042/c DEFINITION ACCESSION REFERENCE AUTHORS JOURNAL VERSION KEYWORDS TITLE COMMENT 셤 셤 g 엄 g ઠે 8 ò ઠ 8

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CTGTTGGAGGAGGCTTTAGGAGGAACAAGAGAAGCAAATCCAGATCGAAATCTACGGTCG 312

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CTGTTGGAGGAGGCTTTTAGGAGGAACAAGAAGCAAATCCAGATCGAAATCTACGGTCG

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GAACTCAAATAAGCAACATGATAAGTGGTATGAGTTCTAGTGGTGGGATCTTGGATGCAT 4712

ACCCTAGGAAGTTTCATAGGTAGGTCAAATCCCGGAGTTTAATTCCAACTTGCCCATCT 4592

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GGAGAATACCTCCATCACAACAAGCTCAGCAATTCCCTTTCTTGATCAACACTACCGGAT 4772

408 GGAGAATACCTCCATCACAACAAGCTCAGCAATTCCCTTTCTTGATCAACACTACCGGAT 349

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singletons were blasted against CDS plus pseudogenes from the TIGRA'S annotation, and the resulting AGI code is presented if more than 90 percent identity was found. The sequences were also blasted against all TIGRA'S introns, and matches longer than 50 pp with 95 percent identity are reported as 'intron found'. The remaining terms for Sequallysis describe the outcome of the evaluation of the CDS detected after pairwise alignment with CDS plus pseudogenes from the TIGRA'S annotation file. The sequences or contigs for which a full CDS with or without STOP codon was detected, a BLASTP against all TIGRA'S protein sequences was performed. Full perfect: 100 percent identity, full good: better than 95 percent identity over more than 95 percent of the sequence; partial good: better than 95 percent identity over less than 95 percent of the sequence; weak similarity: less than 95 percent identity over less than 95 percent of the sequence; no similarity: no hit from BLASTP. Note that the collection contains a few clones for which sequencing was not successful, which could have simple technical reasons. Obviously, information about these clones is missing in the figure found that found the found in the found in the found found have simple technical reasons.
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Seq primer: SeLB GTAACATCAGAGATTTTGAGACAC.
Location/Qualifiers
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7.7%; Score 580; DB
Best Local Similarity 100.0%; Pred. No. 1.2
Matches 580; Conservative 0; Mismatches
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CNSOOPNT RESULT

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2067 ACTITICGGGATAAAAATCICGCCAIGCAAAGGAAITIATITITITICAIGAAAAGGA 2126
CNSOOPNT 528 bp DNA linear GSS 28-JUN-1999
Arabidopsis thaliana genome survey sequence T7 end of BAC F9G12 of
IGF library from strain Columbia of Arabidopsis thaliana, genomic
                                                                                                                                                                                            Bukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta; Bukaryota, Viridiplantae, Streptophyta; Eudicotyledons; core eudicotyledons; spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases I to 528)
Samson, D., Saurin, W., Meissenbach, J. and Quetier, F., Wincker, P., Unpublished
2 (bases I to 528)
                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (25-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
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ive 0; Mismatches 0;
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Bielefeld University, Institute for Genome Research
Universitaetsstrasse 25, D-33594 Bielefeld, Germany
Email: bernd.weisshaar@uni-Pielefeld.de
AGI: AT3G55370; SegAnalysis: truncated in 5' at pos 179;
Translation: no full cds detected
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REGIA, an EU project on functional genomics of transcription factors from Arabidopsis thaliana
Comp. Funct. Genomics 3 (2), 102-108 (2002)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                 CAATGGCGATAATTATAACTATAATACTATGCAAAACGAAACTTTACTTGGGTCATACG
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Definition of the terms used to describe the quality of the clone: The about 2250 sequences from the clone collection were sorted according to clones and clustered. If more than one contig was fargiletons were blasted against CDS plus pseudogenes from the esting sand singletons were blasted against CDS plus pseudogenes from the TIGRYS annotation, and matches longer than 50 bp with 95 percent identity are reported as 'intron found'. The remaining terms for Seqanalysis describe the outcome of the evaluation of the CDS detected after pairwise alignment with CDS plus pseudogenes from the TIGRYS annotation file. The sequences or contigs for which a full CDS with or without STOP codon was detected, a BLASTP against all TIGRYS protein sequences was performed. Pull perfect: 100 percent identity, full good: better than 95 percent identity over less than 95 percent identity over less than 95 percent identity was himiarity; less than 95 percent identity over less than 95 percent of the sequence; weak similarity; less than 95 percent identity over less than 95 percent of the sequence; weak similarity; less than 95 percent identity over less than 95 percent of the sequence; weak similarity; less than 95 percent identity over less than 95 percent of the sequence; obviously, information about these clones for which sequencing was not successful, which could have simple technical reasons.

Determine the collection contains a few clones for which sequencing in the reserved to the sequence of the s
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/ecotype="Columbia"
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/db_xref="taxon:3702"
/clone="006-G10"
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Spermatophyta; Wagnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

I (bases 1 to 433)
Rounsley,S.D., Field,C.E., Bass,S., Linher,K., Linher,K.,
Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Adams,M.D. and
Venter,J.C.
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L Unpublished (1997)
Cother GSSS: F18P187R
Cother GSS: F18P187R
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 0208
Fax: 301 838 0208
Email: rounsley@tigr.org
Seq primer: M3-21
Class: BAC ends
High quality sequence stop: 433.
                                                                                                                                                             TCTTAACAGAGGAATTTTACATCATTCTTAGACTGAACTTTCGGGATAAAAAATCTCGCC
                                                                                                                                                                                              128 TACTATGCAAAACGAAACTTTACTTGGGTCATACCGAGGAAACAAAGGTACACTCGATT
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100.0%; Pred. No. 4.9e-176;
ive 0; Mismatches 0;
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/organism="Arabidopsis thaliana"
/mol type="genomic DNA"
/db xref="Columbia"
/db xref="taxon:3702"
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Nue of a BAC End Sequence Database To Identify Minimal Overlaps for
Arabidopais Genomic Sequencing
Unpublished (1997)
Contact: Steve Genomic Research
Portact: Steve Genomic Research
712 Medical Center Dr., Rockville, MD 20850, USA
The: 301 838 0200
Fax: 301 838 0208
Sea primer: M13-21
Class: BAC ends
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/ecotype="Columbia"
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/clone lib="IGF"
/note="Wector: BeloBACII; Site_1: EcoRI; Site_2: EcoRI;
Produced by Thomas Altmann"
                                TAGGAGGAACAAGAAGAAGCAAATCCAGATCGAAAATCTACGGTCGTGGTCTCGACTGATAA
                                                                                                                                        214 TAGGAGGAACAAGAGAAGCAAATCCAGATCGAAATCTACGGTCGTGGTCTCGACTGATAA
                                                                                                                                                                                                                                                            394 CCTTGGAGATTACAATTCAAGCACACTGGATTAGATTTTGGTGGAACTCAAATAAGCAA
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CK437874 linear EST 29-JUN-2005
GQ0042.BR_P12 GQ004: Non-lignified secondary xylem from mature
trees Picea glauca cDNA clone GenomeQuebec_Id:GQ0042P12 5', mRNA
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1. (bases 1 to 441)

Morency,M.-J., Cooke,J., Pavy,N., Parsons,L., Paule,C., Seguin,A., Retezel,E., Butterfield,Y., Barber,S., Yang,G., Stott,J., Azhorea EST sequencing in Picea glauca (white spruce)

Unpublished (2004)
                                                                                                                                                                                  /clone_lib="IGF"
/note="Vector: BeloBACII; Site_1: EcoRI; Site_2: EcoRI;
Produced by Thomas Altmann"
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Contract: John MacKay
Centre de Recherche en Biologie Forestiere
Universite Laval
Bayillon Charles-Eugene Marchand, Quebec, Quebec, CANADA GIK 7P4
Fax: 418 656 7493
Email: jmacKay@rsvs.ulaval.ca
Center for Computational Genomics and Bioinformatics (CCGB),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTCAACCAATACTAAGTTCTGTTACTTCAATAACTATAGCCTTACTCAACACCTTTT
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                                                                                                                                                                                                                                                                                                                                                                                              12 ACGTGCTCGGATCGCCAAAAGTCCCATTGCCTGAAGCAGCTCTAAAATTGCCCTAGATGGA
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                                                                                                                                                                                                                                                                                                                                                                    4240 ACGTGCTCGGATCGCAAAAGTCCCATTGCCTGAAGCAGCTCTAAAATTGCCCTAGATGTGA
                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                  Length 452;
                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                    4.9%; Score 369; DB 9; I
Similarity 99.8%; Pred. No. 3.6e-160;
19; Conservative 0; Mismatches 1;
                                    1. .452
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/clone="F24E16"
High quality sequence stop: 452.
Location/Qualifiers
                                                                                                                                                              /sex="hermaphrodite"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Picea glauca (white spruce)
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                                                                                                                                                                                                                                                                                                              Best Local Similarity 99.8
Matches 419; Conservative
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CK437874/c
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Arabidopsis thaliana

Rutaryota; Viridiplantes, Streptophyta; Embryophyta; Tracheophyta;

Bukaryota; Viridiplantes, Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnollophyta; eudicotyledons; core eudicotyledons;

rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

E. (Dases I to 452)

Rounsley, S.D., Suh, E.J., Wible, C., Golden, K., Shatsman, S., Choi, P.,

Yu, K., Akinretoye, B., Shen, K., Goonasekaram, S., Militscher, J.,

Adams, M.D. and Venter, J.C.

A BAC End Sequence Database for Identifying Minimal Overlaps in

Arabidopsis Genomic Sequencing. Update 4

Unpublished (1998)

Ocher GSSS: Parinform

Contact: Steve Rounsley

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0200
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/sex="hermaphrodite"
/close_lib="IGF"
/note="Wector: BeloBAGII; Site_1: EcoRI; Site_2: EcoRI;
Produced by Thomas Altmann"
                                                                                                                                                                                                                                                                                                                                                                                                CATGCTAATATCGAGTTTAAACTATTTTTCCAATATAACAACTATTTTCTTTTCGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301 ACGAGAATTATGCACCTAAATTCAGACTAATCCCCCCAAATTTCAGAAATTTATGTATTTT
                                                                                                                                                                                                                                                                                         5519 TATATTAAACGTACTTAAGTCGAATTTTATGACCAAAGTAAATTATGCCGAATGTA
                                                                                                                                                                                                                                                                                                              5459 CTCAATTTCTTGGAGACCCATTATGAGACATTGAGACATCTATAGAACATATATGTAATG
                                                                                                                                                                                                                                   CATGCTAATATCGAGTTTAAACTATTTTTTCCAATATAACAACTATTTTCTTTTCGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 AACTTATATACTCTTATTCTGATTCTTATTTTCTTCTTTTTTAATTCCTTTTTCCTTTCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 AAGACACAAAAAAAAAAAAATACAGAAACGAAAAAAAAGAGATTTTAAAAATTCATAACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACGAGAATTATGCACCTAAATTCAGACTAATCCCCCAAATTTCAGAAATTTATGTATTTT
                                                                                                                                                                     Gaps
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                                                                                                                          Length 433
                                                                                                                      5.0%; Score 382; DB 9; L
99.8%; Pred. No. 3.1e-166;
tive 0; Mismatches 1;
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Seg primer: M13-21
Class: BAC ends
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COMMENT
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AQ011657
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Best Local Similarity 99.7%;
Matches 323; Conservative
                                                                                                                                                                                                                                                                                                        Tel: 517-353-0854
Fax: 517-353-9168
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "note="Organ: Stem from ground to lower part of live crown, on 33 year old tree; Vector: pBluescript II SK (+) KR, Site_1: Eco-RI; Site_2: Xho-I; Tissue was harvested in mid-June, during formation of early wood. cDNA was prepared from 5 mg of poly A+ selected RNA and was diectionmally ligated into the pBluescript II SK (+) XR vector (Stratagene), transformed by electroporation into DH10B cells (In vitrogen) for propagation"
University of Minnesota, MN id Identifier: MNS176207 Clone ID: GQ0042_P12 Clones available through: John MacKay, Ph. D. Professeur adjoint -Assistant professor EMAIL: jmackay@rsvs.ulaval.ca Centre de Recherche en Biologie Forestiere (Forest Biology Research Center) Universite Laval Quebec, Quebec CANADA GIK 7P4
Plate: 2 row: 12 column: P
Seq primer: M13 Reverse Primer.
                                                                                                                                                                                                                                                                                                                        /tissue_type="Non-lignified differentiating secondary xylem from normal vertical trees"
/dev stage="Non-lignified secondary xylem from trees
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/lab_host="E. coli DH10B cells"
/clone_lib="GQ004: Non-lignified secondary xylem from mature_trees"
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28394 Lambda-PRL2 Arabidopsis thaliana CDNA clone 104F10XP 3', mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       169 TTTCGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGGTTCCCGATATTACCC 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
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                                                                                                                                                                                                   /organism="Picea glauca"
|mol_trype="mRNA"
|strain="Two trees of provenance 5333 and one from 5206"
|db_xref="taxon:3330"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6370 TITCGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGGTTTCCCGATATTACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6190 AGATATCACATCAATCCACTTGCTTTGAAGACGTGGTTGGAACGTCTTTTTTCCACGA
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100.0%; Pred. No. 1e-138;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                     /clone="GenomeQuebec_Id:GQ0042P12"
/sex="Hermaphrodite"
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                                                                                                                                                      Location/Qualifiers
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AA585745.1 GI:2393157
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Best Local Similarity 100.
Matches 323; Conservative
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AA585745
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/mol type="mcNnh"
/ecotype="Columbia"
/ecotype="Columbia"
/db xref="taxon:3702"
/clone="104FlOXP"
/clone="The transport of the transport of tran
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 446)

Newman, T., deBruijn, F.J., Green, P., Keegstra, K., Kende, H.,

McIntosh, L., Ohlrogge, J., Raikhel, N., Somerville, S., Thomashow, M.,

Retzel, E. and Somerville, C.

Genes galore: a summary of methods for accessing results from

large-scale partial sequencing of anonymous Arabidopsis cDNA clones

Plant Physiol. 106, 1241-1255 (1994)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: 22313cra@ibm.cl.msu.edu
The sequence entry for this EST has been reverse complimented and
is being submitted in the sense orientation.
Seq primer: M13 -21 dye primer.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Thomas Newman
MSU-DOE Plant Research Laboratory
Michigan State University
MSU-DOE-PRE, Michigan State University, Plant Biology Bldg., E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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/note="Weetor: pBACWICH; Site_1: HindIII; Site_2: HindIII;
/note="weetor" pBACWICH; Site_1: HindIII; Site_2: HindIII;
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blast is an important model fungal phosen for studying
numerous aspects of the fungal-host interaction. In
order to facilitate genome wide analysis, a BAC library
containing 9216 clones with an average insert size of 130
kbp was constructed. This library represents greater
than 25X genome coverage. High density colony filters
are available upon request."
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AQ361936 AQ361936 GI:4211775
GSS.
Magnaporthe grisea (anamorph: Pyricularia grisea)
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                                                                                                                                                   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe. . (bases 1 to 199)
Yu, Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R., Phillips, K., Sasinowski, M. Wing, R.A. and Dean, R.A.
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                                                                                                                                                                                                                                                                                                                                                                                            clemson University
100 Jordan Hall, Clemson University, Clemson, SC 29634
Tel: 864 655 5737
Fax: 864 656 4293
Email: rdeam@clemson.edu
Class: RAC ends
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                                                                                                       Magnaporthe grisea (anamorph: Pyricularia grisea)
Magnaporthe grisea
clone mgxb0004F23f, genomic survey sequence.
AQ361597
                                                                                                                                                                                                                                                                                                                                                 Contact: Dean RA
Clemson University Genomics Institute
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Location/Qualifiers
                                                       AQ361597.1 GI:4211436
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/clone_lib="CUGI Rice Blast BAC Library of a haploid genome (n=7) of approximately 40 Mbp. Rice blast is an important model fungal pathogen for studying numerous aspects of the fungal-host interaction. In order to facilitate genome wide analysis, a BAC library containing 9216 clones with an average insert size of 130 kbp was constructed. This library represents greater than 25X genome coverage. High density colony filters are available upon request."
                                                                                                 1 (bases 1 to 492)
Yu, Y., Zhu, H., Boyd,C.A., Gaudette,B., Gayle,A., Kingsbury,R.,
Phillips,K., Sasinowski,M. Wing,R.A. and Dean,R.A.
A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
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                                     Sordariomycetes;
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Magnaporthe grisea
Eukaryota; Pungi; Ascomycota; Pezizomycotina; Sordariomycetes
Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
                                                                                                                                                                                                                                                                                Context: Dean RA
Clemson University Genomics Institute
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson University, Clemson, SC 29634
Tel: 864 656 5737
Fea: 864 656 4293
Email: rdeamodlemson.edu
Seq primer: TARTACGACTCACTATAGGG
Class: BAC ends
High quality sequence stop: 75.
Location/Qualitiers
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Best Local Similarity 99.3%; Pred. No. 9.9e-34;
Matches 148; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Magnaporthe grisea"
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CAAAGCTAGCTAGATTTTTCTCAAGTGAGCAACAGTCTAATTCTTCTGAAAAAACTTGTT 360
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Sequence 3, Appli
Sequence 1, Appli
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Sequence 2767, Apple Sequence 2767, Apple Sequence 2767, Apple 269, Apple 2690, Apple 2690,
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409, App
196, App
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Sequence 3563, Ap
Sequence 3663, Ap
Sequence 46, Appl
Sequence 1, Appli
Sequence 1, Appli
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2: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

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Sequence 1, Application US/10650249
Publication No. US20040045055A1
GENERAL INFORMATION:
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TILLE OF INVENTION: THE GENE FOR A DOF TRANSCRIPTION FACTOR CAPABLE OF ALTERING
TITLE OF INVENTION: THE SIZE AND STATURE OF A PLANT
FILE REPERRINCE: WSHU 2064.1
CURRENT APPLICATION NUMBER: US/10/650,249
PRIOR RILING DATE: 2003-08-02
PRIOR PILING DATE: 2003-08-02
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### Matches 1402; Conservative 0; Mismatches 0; Indels 0; Gaps 0; 6238 e119 GTTTCGGATCTAGATATCACATCACTTGCTTTGAGACGTGGTTGGAACGTCTTC 6238 e1249 GTTTCGGATCTAGATATCACATCACTTGCTTTGAAGACGTGGTTGGACGTCTTC 4190 e239 TTTTCCACGATGTTCCTCGTGGGTGGGGTCCATCTTTGAGACGTCTTCGTGGTGGGGGTCTTC 4190 e1189 TTTTCCACGATGTTCCTCGTGGGTGGGGTCCATCTTTGGGACCACTGTCGGTAGAGG 130 e239 ATCTTGAAGGATAGCCTTTCTTATCGCAATGACGATTGTAGAGGATCCTTTATCGAATGACGATTCCTTTATCGCAATGACGATTGTAGAGCCATCTCCT 6358 e1180 e1181	6359 TTCTACTGTCCTTTCGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGGTTTCC 6418 4069 TTCTACTGTCCTTTCGATGAAGTGACAGATAGCTGGGCAATGGAATCCGAGGAGTTTCC 4010 6419 CGATATTACCTTTGTTGAAAAGTCTCAATAGCCCTTGGTCTTCTGAGACTGTATCTT 6478 4009 CGATATTACCCTTTGTTGAAAAGTCTCAATAGCCCTTTGTGGACTGTATCTTT 3950	6479 GATATTCTTGGAGTAGACGAGAGTGTCGTGCTCCACCATGTTGGGGATCTAGATATCACA 6538		6719 GTGACAGATAGCTGGCAATGGAATCCGAGGGGGTTTCCCGATATTACCCTTTGTTGAAA 6778	6839 AGTGTCGTGCTCCACCATGTTGGGGATCTAGATATCACATCCATTGCTTTGAAGA 6898		7079 GAATCCGAGGAGTTTCCCGATATTACCCTTTGTTGAAAAGTCTCAATAGCCTCTGGTC 7138	3289 TTCTGAGACTGTATCTTTGATATTCTTGGAGTAGACGAGAGTGCTGCTCCACCATGTT 3230 7199 GGGGATCTAGATATCACATCCACTTGCTTTGAAGACGTGGTTGGAACGTCTTCTTT 7258
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55 11 12 12 56	Qy 5693 TTTCCCAAGACAAAAAAAAAAAAATACAGAAAAAAAGAGATTTTAAAAATTCA 5752 Db 1261 TTTCCCAAGACACAAAAAAAAAAAAACAGAAACGAAAAAAGAGATTTTAAAAATTCA 1320 Qy 5753 TAACCCACGAGAATTATGCACCTAAATTCAGACTAATCCCCCCAAATTTATG 5812 Db 1321 TAACCCACGAGAATTATGCACCTAAATTCAGACTAATCCCCCCAAATTTCAGAAATTTATG 1380	Oy 5813 TATTTTGCGATTTAATATTGTGTTCACAATGCCAACTAACT	1501 ACCAATAGACTATCATCATTAGTTAATGCATGATCTATAATGTATTTTTAGA 5993 GATATGTCATTTATCTGGATATAAAGATGGCGTTTTAACCTACTATGCAATTTTTC 1561 GATATGTCATTTATCTGGATATAAAGATGGCGTTTTAACCTACTTTGCAATTTTTC 1561 GATATGTCATTTATCTGGATATAAAGATGGCGTTTTAACCTACTTTGCAATTTTTC 1661 AATATGTCATTTATCTGGATATAAAGATGGCGTTTTAACCTACTTTGCAATTTTTC	ATCITTCITCTATACATAGATCAATACACTTTGTTTTTAAAAGAAATTAAAAACTTA 168 ATCITTCITCTAATACATAGATCAATACACTTTGTTTTTTTAAAAGAAATTAAAAACTTA 168 TTTCAAACATCGATCACATTTTTACTTTTGTTTCCATATTGACTACATTTATAGGCTCAC 617 TTTCAAACATCGATCACATTTTTACTTTTGTTTTCCATATTGACTACATTTATAGGCTCAC 174	Oy 6173 ACTIT 6178 Db 1741 ACTIT 1746 RESULT 3	GENERAL INFORMATION: US20020133848A1; Publication No. US20020133848A1; GENERAL INFORMATION: APPLICANT: Exelixis Plant Sciences, Inc.; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF AN ANTHOCYANIN MUTANT (ANT TITLE OF INVENTION: TOWATO FILE REFERENCE: EP01-002C CURRENT APPLICATION NUMBER: US/10/033,190 CURRENT FILING DATE: 2001-10-29	PRIOR APPLICATION NUMBER: US 60/244,685 ; PRIOR FILING DATE: 2000-10-30 ; NUMBER OF SEQ ID NOS: 5 ; SOFTWARE: Patentin version 3.1 ; SEQ ID NO 3 . I.ENGTH. 10078	TYPE: DNA 7 TYPE: DNA 7 ORGANISM: pAG3202 US-10-033-190-3 US-10-033-190-3 US-10-031-190-3 US-10-031-190-3 18.5%; Score 1402; DB 5; Length 10078; Best Local Similarity 100.0%; Pred. No. 0;

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APPLICANT: Wadner, Ry
APPLICANT: Mathews, Helma
APPLICANT: Mathews, Helma
APPLICANT: Mathews, Wency J.
TITLE OF INVENTION: TRAIT-ASSOCIATED GENE IDENTIFICATION
TITLE OF INVENTION: METHOD
FILE REFERENCE: 4257-0018.30
CURRENT FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: US 60/124,232
PRIOR PLING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FABELSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                    CGGCCGCCACCGCGGTGGAGCT 7580
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US-09-522-334-1/c
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Sequence 20, Application US/10650249

| Sequence 20, Application US20040045055A1
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| TITLE OF INVENTION: THE GENE FOR A DOF TRANSCRIPTION PACTOR CAPABLE OF ALTERING
| TITLE OF INVENTION: THE SIZE AND STATURE OF A FLANT
| TITLE OF INVENTION: THE SIZE AND STATURE OF A FLANT
| TITLE OF INVENTION: THE SIZE AND STATURE OF A FLANT
| CURRENT APPLICATION NUMBER: US/10/650,249
| CURRENT APPLICATION NUMBER: US/10/650,249
| PRIOR PILING DATE: 2002-08-02
| NUMBER OF SEQ ID NOS: 20
| SEQ ID NO 20
| SOFTWARE: PatentIn version 3.1
| SEQ ID NO 20
| LENGTH: 1062
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Matches 1062; Conservative 0; Mismatches
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                                                                          Sequence 17, Application US/10650249
Publication No. US20040045055A1
GRNERAL INFORMATION:
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TITLE OF INVENTION: THE GIZE AND STATURE OF A PLANT
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TITLE OF INVENTION NUMBER: US/10/650,249
CURRENT FILING DATE: 2002-08-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE PARENT VERSION 3.1
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ORGANISM: Arabidopsis thaliana
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FILE REFERENCE: WSHU 2064.1

CURRENT APPLICATION NUMBER: US/10/650,249

CURRENT FILING DATE: 2003-08-28

PRIOR APPLICATION NUMBER: US 60/406,657

PRIOR FILING DATE: 2002-08-02

NUMBER OF SEQ ID NOS: 20

SOFTWARE: Patentin version 3.1

SEQ ID NO 19
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3104 3164 3344 3404 3464 3584 3644 3764 ö 3524 300 480 720 840 301 CTCTCTCTCTCTAGATCAATTCTTTCTATCATGATGATGATTATCCACCATATCTGCGACC 361 TCTTACCTAAAAAGGATACAAGTAAGAGATTCAAAGATGGTTTTCTCACATCTCTCCAGTG GTTTCTGATTCGTTCCTTTTTTCCTCCAAGCTCGATCAAGATTTATGAAAATTTGATGAGA ACAAAAAGAAATAAAGAGCCTAAGAGAATGAAAAATTGAAAGAGAAAAAGAGCATTG 121 ACAAAAAGAAATAAAGAGCCTAAGAGAATGATGAAAATTGAAAGAGAAAAAAGAGCATTG CTCTCTCTCTAGATCAATTCTTTCTTCTATGATGTGATTATCCACCATATCTGCGACC TCTTACCTAAAAAGGATACAAGTAAGAGATTCAAAGATGGTTTTCTCATCTTCCAGTG **AATCAGTTCGATTCCCAAAATTGGCAGCAGGTAAAAATCAGTTTATGATATTTGCTAGAT** GITTCTGATTCGTTCCTTTTTCCTCCAAGCTCGATCAAGATTTATGAAAATTTGATGAGA TTAGTTGATTAAACCCTTTTTTTTTTTTTCTTCTCGAATATACGAAAATATAAAAGAT TTATAGAAAAGAAAAAAAGAGAGAGTAAAGAGAATTAAGAAACACAATAAATTAAACAA TAAAAACCTTTTTTTCTTGTCTTCTCCAAGGGCTTATGTATAATGTTTTTCTTACAGGATT ö Indela 3765 721 3825 781 ò 셤 셤

ALTERING

Sequence 19, Application US/10650249
Publication No. US20040045055A1
GENERAL INFORMATION:
APPLICANT: Neff, Michael M
TITLE OF INVENTION: THE GENE FOR A DOF TRANSCRIPTION FACTOR CAPABLE OF
TITLE OF INVENTION: THE SIZE AND STATURE OF A PLANT

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Sequence 15, Application US/10650249
; Publication No. US20040045055A1
; Publication No. US20040045055A1
; GENERAL INFORMATION:
; APPLICANT: Neff, Michael M
; TITLE OF INVENTION: THE GENE FOR A DOF TRANSCRIPTION PACTOR CAPABLE OF ALTERING
; TITLE OF INVENTION: THE SIZE AND STATURE OF A PLANT
; FILE REFERENCE: WSHU 2064.1
; FILE REPERENCE: WSHU 2064.1
; CURRENT APPLICATION NUMBER: US/10/650,249
; CURRENT FILING DATE: 2003-08-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 15
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                                                                                                                                                         5012 AATATCAACATAAACTCAGGCAGGAACGAGGAATACACATCATGGGGGAGGTAACAGTTCT
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                            TTGGTGCAATCTTCAAACGCGTTATATCCATTACTAGAAGGTAAGGGAGGTGTTAATCAA
                                                                                                                                                                                                        GATITITICITICAGGCGGGGTTAGCGCCACGAAACAAGAAATGTGAAGGCGGAAGAAT
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9.0%; Score 684; DB 7; Length 684;
Best Local Similarity 100.0%; Pred. No. 1.3e-298;
Matches 684; Conservative 0; Mismatches 0; Indels
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US-10-650-249-15
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Publication No. US20040045055A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: THE GENE FOR A DOF TRANSCRIPTION FACTOR CAPABLE OF ALTERING
TITLE OF INVENTION: THE SIZE AND STATURE OF A PLANT
TITLE OF INVENTION: THE SIZE AND STATURE OF A PLANT
TITLE OF INVENTION: THE SIZE AND STATURE OF A PLANT
TITLE OF INVENTION UNMER: US/10/650,249
CURRENT APPLICATION NUMBER: US 60/406,657
PRIOR APPLICATION NUMBER: US 60/406,657
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PARENT IN VERSION 3.1
SEQ ID NOS: 20
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301 AACCCTAGGAAGTTTCATAGCTACGGTCAAATCCCGGAGTTTAATTCCAACTTGCCCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       361 TIGCCTCCTCTCCAAAGCCTTGGAGATTACAATTCAAGCAACACTGGATTAGATTTTGGT
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1 AIGGIGGAACGIGCTCGGAICGCAAAGICCCAITGCCTGAAGCAGCICTAAAITGCCCT
                                                                TGAAAAACTATAATTAATCTGCAATTCTTGTCAAAGTAGTCACAATTTTTATCTATTTTC
                                                                                  TTTTGTCTCCGACCAATGTTTCAAACTCGAATCCTTTCGTTAAAAGTTGTTTCTGCTTTA
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                                                                                                                                                                                            ; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-650-249-12
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Best Local Similarity 100.0
Matches 888; Conservative
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US-10-650-249-12
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GENERAL INFORMATION:

APPLICANT: RATCLIFFE, Oliver
APPLICANT: RATCLIFFE, Oliver
APPLICANT: RATCLIFFE, Oliver
APPLICANT: ALGENAMIN, JOSE Luis
APPLICANT: ALGENAMIN, JOSE Luis
APPLICANT: ALGORI, Luc J
APPLICANT: DUBELL, Arnold T
APPLICANT: HEARD, Jacqueline E
APPLICANT: HEARD, Jacqueline E
APPLICANT: PIGAIM, MAREHA L
APPLICANT: REUBER, T Lynne
APPLICANT: Vid-G-Liang
APPLICANT: WIGHTON YIE-d-Related Polynucleotides and Polypeptides in Plants
TITLE OF INVENTION YIE-d-Related Polynucleotides and Polypeptides in Plants
FILE REFERENCE: MBI0036-2 US
CURRENT FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/316,049
PRIOR FILING DATE: 2001-04-18
PRIOR FILING DATE: 2001-10-05
PRIOR FILING DATE: 2001-10-10
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                                              126 CGCCATTTCTGCAAAACATGTCGTCGCTATTGGACACGTGGCGGTTCCTTGAGGAATGTT 185
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                                                                                                  CCTGTTGGAGGAGGCTTTAGGAGGAACAAGAGAAAGAAAATCCAGATCGAAATCTACGGTC
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; Publication No. US20030226173A1
; GENERAL INFORMATION:
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US-10-225-066A-409
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Sequence 7187, Application US/10487901

Publication No. US20050091708A1

GENERAL INPORMATION:
APPLICANT: Oreido, Jeremiah Vincent
APPLICANT: Miller, Barbara
APPLICANT: Miller, Barbara
APPLICANT: Miller, Barbara
APPLICANT: Blakeslee, Beth
APPLICANT: Blakeslee, Beth
APPLICANT: Blakeslee, Beth
APPLICANT: Shukla, Vipula
APPLICANT: Crosley, Rodney
TITLE OF INVENTION: Nucleic Acid Compositions Conferring Altered Metabolic Characteri
FILE REFERENCE: DOW-08552

CURRENT APPLICANT: 2004-02-26

NUMBER OF SEQ ID NOS: 7560

SOFTWARE: PatentIn version 3.1

LENGTH: 645
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                                                                                                                                            GATTATTCCAATCAGCTAATGTTTAAGCCCTTGATGGATTTTTTCTTCAGGCGGGGTTAGC
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Best Local Similarity 100.0%; Pred. No. 5.7e-252;
Matches 581; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Synthetic US-10-487-901-7187
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US-10-487-901-7187
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                                                                                                 1 Argeregaacerecregarcecaaaagrecearrecereaageagereraaarrecer
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                                  0; Gaps
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; Sequence 2767, Application US/10374780A
; Publication No. US20040019927A1
; GENERAL INFORMATION:
APPLICANT: Sherman, Bradley K
APPLICANT: Riechmann, Jose Luis
APPLICANT: Heard, Jacqueline E
APPLICANT: Ratcliffe, Oliver
APPLICANT: Ratcliffe, Oliver
APPLICANT: Reubert A
APPLICANT: Reubert James
APPLICANT: Reubert James
APPLICANT: Reubert James
APPLICANT: Pelgrim, Marsha L
APPLICANT: Pineda, Omais
APPLICANT: Pineda, Omais
APPLICANT: Pineda, Omais
APPLICANT: Vu, Guo-Liand T
APPLICANT: Vu, Guo-Liand T
APPLICANT: Vu, Guo-Liand T
APPLICANT: Vu, Guo-Liand T
APPLICANT: Vu, Guo-Liand S
FILE REFRERENCE: MBL 003-02-25
FRICE REPRENCE: MBL 09/837,944
; FRICK FILING DATE: 2001-04-18
; FRICK FILING DATE: 2001-04-18
; FRICK FILING DATE: 2001-04-18
Length 795;
 Query Match 7.7%; Score 581; DB 6; Length 79
Best Local Similarity 100.0%; Pred. No. 5.8e-252;
Matches 581; Conservative 0; Mismatches 0; Indels
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PRIOR APPLICATION NUMBER: 09/934,455
PRIOR FILING DATE: 2001-08-22
PRIOR PPLING DATE: 2001-11-19
PRIOR PILING DATE: 2001-11-19
PRIOR PILING DATE: 2001-11-19
PRIOR PILING DATE: 2001-12-11
PRIOR APPLICATION NUMBER: 10/17,468
PRIOR APPLICATION NUMBER: 10/17,468
PRIOR PILING DATE: 2002-06-14
PRIOR PILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: 10/25,067
PRIOR PILING DATE: 2002-08-09
PRIOR PILING DATE: 2002-08-09
PRIOR FILING DATE: 2002-08-09
PRIOR FILING DATE: 2002-08-09
PRIOR FILING DATE: 2002-08-09
PRIOR FILING DATE: 2002-08-09
NUMBER OF SEQ ID NOS: 2906
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; Sequence 409, Application US/10225066A
; Publication No. US20050160493A9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Arabidopsis thaliana
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COTHER INFORMATION: G1906
US-10-374-780A-2767
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 2767
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4351

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CAAAGGCTAATTTTGAGGCTCAAAGGAAAGGTATGGTTATAAAACTATCTTTTTGATCTT 5285
GTACATTGGTGCTTGTCATGCGAGTTATTGCTGAGGAAGATCAAACCATGCAGCTATATTC 300
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APPLICANT: Davis, Keith R.
APPLICANT: Allen, Keith
APPLICANT: Hoffman, Neil
APPLICANT: Hurban, Patrich
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TITLE OF INVENTION: Davis 100/170,152
CURRENT APPLICATION NUMBER: 00/178,503
PRIOR FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 999
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 196
TENCENT: 77
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100.0%; Pred. No. 3.7e-250;
tive 0; Mismatches 0;
                                                                                                                                                                                                      Sequence 196, Application US/09770152 Publication No. US20020040489A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                            Matthew, Abraham V.
Ledford, Brooke L.
Woessner, Jeffrey P.
Haas, William David
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                                                                                                                                                                                                                                                                                        An, Yong-Qiang
Hamilton, Carol M.
Price, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                    Yu, Yang
Rameaka, Joshua G.
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Kricker, Maja
Slader, Ted
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Best Local Similarity 100.(
Matches 577; Conservative
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US-09-770-152-196
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                                                                                          APPLICANT: ALMA, LUC J
APPLICANT: ALMA, LUC J
APPLICANT: ALMA, LUC J
APPLICANT: HEARD, Jacqueline E
APPLICANT: FILGARM, Marsha L
APPLICANT: FILGARM, Marsha L
APPLICANT: TANG, Cai-Zhong
APPLICANT: GREELMAN, Robert A
APPLICANT: GREELMAN, Robert A
APPLICANT: REUBER, T. Lynne
APPLICANT: WO Guo-Liang
APPLICANT: WO Guo-Liang
TITLE OF INVENTION: Yield-Related Polynucleotides and Polypeptides in Plants
FILE REFERENCE: MBI0036-2 US
TITLE OF INVENTION: Yield-Related Polynucleotides and Polypeptides in Plants
FILE REFERENCE: MBI0036-2 US
CURRENT APPLICATION NUMBER: 05/02-06-09
FRIOR FILING DATE: 2001-04-18
FRIOR FILING DATE: 2001-08-09
FRIOR FILING DATE: 2001-12-05
FRIOR FILING DATE: 2001-12-11
FRIOR FILING DATE: 2001-12-11
FRIOR FILING DATE: 2001-12-11
FRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 1122
SUPPLYMARE: PatentIn version 3.1
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                    Mendel Biotechnology,
RATCLIFFE, Oliver
RIECHMANN, Jose Luis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Arabidopsis thaliana
US-10-225-066A-409
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LENGTH: 795
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Sequence 3563, Application US/09938842A

Patent No. US20020160378A1

GENERAL INFORMATION:

APPLICANT: Harper, Jeff

APPLICANT: Wang, Xun

FILE REFRENCE: SCRIP1300-3

CURRENT APPLICATION NUMBER: US 60/227, 866

PRIOR PILING DATE: 2001-08-24

PRIOR PLING DATE: 2001-01-16

PRIOR PLING DATE: 2001-01-16

PRIOR PLING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-06-22

NUMBER OF SEQ ID NOS: 5379

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Best Local Similarity 100.0%; Pred. No. 1.9e-155;
Matches 368; Conservative 0; Mismatches 0;
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US-09-938-842A-3563
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US-09-938-842A-3563
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